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(54) DNA STRAND USEFUL IN INCREASING CAROTENOID YIELD

(57) A DNA chain having characteristic of increasing carotenoid production, and containing the nucleotide sequence which encodes the polypeptide having the substantially same amino acid sequence described in SEQUENCE ID No. 1 or 2, or a DNA chain which hybridizes with said DNA chain, and a method for production for carotenoid characterized by introducing said DNA chain into the carotenoid-producing microorganisms, culturing said transformed microorganism and increasing carotenoid content in the culture broth and cells.

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Description

FIELD OF THE INVENTION

5 The present invention relates to a DNA chain which provides higher carotenoid content during biosynthesis of carotenoid and a method for producing carotenoids characterized by introducing said DNA chain into carotenoid producing microorganism to express said chain and to obtain higher carotenoid content.

BACK GROUND OF THE INVENTION

10 Carotenoid is a general name of a kind of natural pigments. Generally, carotenoids have 40 carbon atoms and consists of isoprene skeletons, and Carotenoids are abundant in the natural world. Approximately 600 kinds of carotenoids have been isolated and identified up to the present [(see Key to carotenoids. Basel-Boston, Birkhauser, 1987(Pfander, H. ed.)). Carotenoids are synthesized through the isoprenoid biosynthetic pathway, a part of which is common to the pathways for steroids and other terpenoids. Passing through the isoprene common biosynthetic pathway, hydroxymethylglutaryl-CoA(HMG-CoA) is converted to isopentenyl pyrophosphate(IPP), which has 5 carbon atoms, via mevalonate. Then IPP is converted to dimethylallyl pyrophosphate(DMAPP) by isomerization. Then, by polycondensation with IPP which has 5 carbon atoms, DMAPP is converted sequentially to geranyl pyrophosphate(GPP which has 10 carbon atoms), farnesyl pyrophosphate (FPP which has 15 carbon atoms), geranylgeranyl pyrophosphate(GGPP which has 20 carbon atoms) and so forth (Figure 1).

20 The carotenoid biosynthetic pathway is branched from the isoprene common pathway at the point of GGPP is formed. At the point, two molecules of GGPP are condensed to synthesize phytoene which is the first carotenoid and colorless. Then, phytoene is converted to lycopene by desaturation reaction. Then, lycopene is converted to β -carotene by cyclization. Various xanthophylls such as zeaxanthin and astaxanthin are synthesized by introducing hydroxyl groups or keto groups to β -carotene.

25 Recently, the inventors of the present invention cloned the carotenoid biosynthesis genes derived from *Erwinia uredovora*, which is a non-photosynthetic epiphytic bacterium in *Escherichia coli* by using yellowish color of *Er. uredovora* as markers and elucidated the functions of the genes. Then, various combinations of these genes are introduced to express, and it made possible that microorganisms such as *E. coli* and yeast produce phytoene, lycopene, β -carotene, zeaxanthin and so forth(See Figure 2): [See Misawa, N., Nakagawa, M., Kobayashi, K., Yamano, S., Izawa, Y., Nakamura, K. and Harashima, K., "Elucidation of the *Erwinia uredovora* carotenoid biosynthetic pathway by functional analysis of gene products expressed in *Escherichia coli*", J. Bacteriol., 172: 6704-6712 (1990); Misawa, N., Yamano, S., and Ikenaga, H., "Production of β -carotene in *Zymomonas mobilis* and *Agrobacterium tumefaciens* by introduction of the biosynthesis genes from *Erwinia uredovora*", Appl. Environ. Microbiol., 57: 1847-1849 (1991); Yamano, S., Ishii, T., Nakagawa, M., Ikenaga, H., and Misawa, N., "Metabolic engineering for production of β -carotene and lycopene in *Saccharomyces cerevisiae*", Biosci. Biotech. Biochem., 58: 1112-1114 (1994) and Japanese Patent Application laid-open No. HEI 3-58786(Japanese Patent Application filing No. HEI 2-53255): "A DNA chain useful for synthesis of carotenoids" by the inventors of the present invention]. With the carotenoid biosynthesis genes from *Er. uredovora*, carotenoids can be synthesized from FPP. Since FPP is the common substrate not only for carotenoids but also for steroids and other terpenoids, bacteria incapable of synthesizing carotenoids also have FPP. Accordingly, for example, when four *crt* genes, *crtE*, *crtB*, *crtI* and *crtY*, which are necessary for biosynthesis of β -carotene from FPP are introduced in microorganisms, the microorganism becomes capable of producing β -carotene (See Figure 2). Furthermore, by the same procedures as mentioned above, the inventors cloned the carotenoid biosynthesis genes derived from a marine bacterium, *Agrobacterium aurantiacum* in *E. coli*. By expressing various combinations of the genes from the bacterium and those from the above-mentioned *Er. uredovora*, it made possible that the microorganisms such as *E. coli* produce astaxanthin, canthaxanthin and so forth (See Figure 3): (Norihiko Misawa et al., "Elucidation of an astaxanthin biosynthetic pathway at the level of the biosynthesis genes", Abstract of the 36th Symposium on the chemistry of natural products: 175-180 (1994)). Among the above carotenoids, astaxanthin, zeaxanthin and β -carotene are already in practical use and are regarded as promising substances. They are used for food or feed additives as red or yellow natural coloring agents or as nutritional aid having cancer prophylactic activity, immunopotentiating activity or provitamin A activity. Accordingly, when the carotenoid biosynthesis genes obtained by the inventors is used as exogenous genes for transforming microorganisms such as *E. coli* to express, it gave microorganisms such as *E. coli* the capability of biosynthesis for producing useful carotenoids. Up to now, it is the only way to improve production of useful carotenoids was to find out microorganism which can synthesize sufficient amount of a targeted carotenoid, and to try to increase its production by investigating culture conditions or mutation treatment. Owing to the studies done by the inventors, it became possible to choose host microorganism which is cultured easily and proliferates rapidly, and is guaranteed to be safe for food regardless of its carotenoid producing capability. As a matter of course, it is also possible to use microorganisms which can synthesize sufficient amount of useful carotenoids originally. In such a case, by transforming the microorganisms with carotenoid biosynthesis genes, it became possible to obtain higher carotenoid production or to alter final caroten-

oid products. For example, when both *cr1W* and *cr1Z* genes from *Ag. aurantiacum* were introduced into a microorganism capable of producing β -carotene as a final product to express them, the microorganism was transformed to another one which produce astaxanthin as a final product.

On the other hand, both astaxanthin and β -carotene can also be synthesized by organic synthesis methods. In these cases, considering these carotenoids are used for feed or food additives, there is problems that by-products are also produced and such synthetic products are not preferred by consumers because they prefer natural products. However, carotenoids produced by the conventional fermentation methods could not compete with those by the organic synthesis methods in price. As mentioned earlier, when the above mentioned carotenoid biosynthesis genes are used, it improves the fermentation methods, thereby it is considered that the carotenoid produced by the fermentation methods will be able to compete with those by the organic synthesis methods in price. If the microorganism can accumulate enough amount of carotenoid in itself, the carotenoid produced by the microorganisms will succeed in such price competition. Therefore, a technology to obtain higher carotenoid content by using microorganisms has been longed for.

Until now, in order to obtain higher carotenoid production in its biosynthesis; the traditional random mutation method is only employed to select mutant strains having higher carotenoid content with mutagenic agent such as NTG. However, this method requires huge amount of time and labor of technicians. In addition, even if enhancement of carotenoid synthesis is successfully achieved, the method requires both huge amount of time and effort to inhibit decreasing of carotenoid content caused by frequent reverse mutations naturally happens because the method lacks its theoretical basis.

SUMMARY OF THE INVENTION

The object of the present invention is to increase amount of carotenoids biosynthetically produced by microorganisms.

To solve the above problem, the inventors have investigated the problem thoroughly and developed a novel technology which provides several times higher carotenoid production amount by introducing a DNA chain containing only one gene into a carotenoid producing microorganism to express the gene in them.

More specifically, the inventors of the present invention found the followings and completed the present invention. When a DNA chain containing a gene substantially encoding an amino acid sequence of IPP isomerase which converts IPP into DMAPP, is introduced in microorganisms such as *E. coli* having carotenoid synthesis gene derived from *Er. uredozora* and so forth, content of carotenoid in cells such as lycopene and β -carotene becomes 1.5-4.5 times higher than that in control cells can be achieved. The gene substantially encoding IPP isomerase amino acid sequence which converts IPP into DMAPP was obtained from the astaxanthin producing microorganisms such as *Phaffia rhodozyma* and *Haematococcus pluvialis*.

The characteristics of the DNA chain of the present invention are as follows.

(1) A DNA chain capable of increasing carotenoid production amount and containing the nucleotide sequence which encodes the polypeptide having the amino acid sequence substantially shown in Sequence ID No. 1, or a DNA chain that can be hybridized with said DNA chain.

(2) A DNA chain capable of increasing carotenoid production and containing the nucleotide sequence which encodes the polypeptide having the amino acid sequence substantially shown in Sequence ID No. 2, or a DNA chain that can be hybridized with said DNA chain.

The present invention also relates to a method for carotenoid production. The characteristics of the carotenoids production methods of the present invention are as follows.

(3) A production method characterized by introducing the DNA chain mentioned above either (1) or (2) into carotenoid producing microorganism, culturing said transformed microorganism and increasing carotenoid content in the cells and culture broth.

(4) A production method characterized by introducing the DNA chain containing the nucleotide sequence which encodes the polypeptide having the substantially same amino acid sequence shown in Sequence ID No. 3, or a DNA chain that can be hybridized with said DNA chain into carotenoid producing microorganism, culturing said microorganism and increasing carotenoid content in the cells and culture broth.

The present invention is described herein below.

As described in before, by introducing the carotenoid biosynthesis gene derived from microorganisms such as *Erwinia uredozora*, the non-photosynthetic soil bacteria and *Agrobacterium aurantiacum*, the marine bacteria) into other microorganisms which do not produce carotenoids such as *E. coli*, the microorganism can produce useful carotenoids such as astaxanthin, zeaxanthin, β -carotene and lycopene. In order to compete in price of the carotenoid produced by using the organic synthesis methods, it is necessary to achieve as higher carotenoid production as possible. The IPP isomerase gene, which include the gene encoding the polypeptide whose amino acid sequence is substantially IPP isomerase, of the invention is extremely useful for increasing the production amount of carotenoids. By using mod-

ern biotechnology, it is relatively easy to increase production amount of a protein encoded by an exogenous gene by enhancing expression level of the gene. However, if amounts of substrate necessary for a protein, that is enzyme, is limited, higher production of the protein does not lead to higher production of biochemicals such as carotenoids. For example, without sufficient amount of FPP, which is the first substrate, enhancement of expression level of the carotenoid synthesis genes does not lead to higher amount of carotenoids production. This time, we succeeded in increasing carotenoid production amount by introducing the IPP isomerase gene. It is considered that the introduction of the IPP isomerase gene makes the flow of, the upstream of the pathway up to FPP larger (more efficient) and consequently, increased supply of FPP led to higher carotenoid production amount. The present invention started from the findings that by introducing either the gene encoding IPP isomerase, which convert from IPP to DMAPP vice versa, or encoding the protein homologous to IPP isomerase into carotenoid producing microorganism such as *E. coli*, to express the gene, carotenoid production amount is increased. By using carotenoid biosynthesis genes from *Er. uredovora*, cDNA expression libraries of *Phaffia rhodozyma*, *Haematococcus pluvialis* and so forth were prepared in β -carotene producing *E. coli* as a host. As increased β -carotene content in *E. coli* made, some of the yellowish colonies brighter till almost orange. The plasmids extracted from such *E. coli* colonies were analyzed and were found to have genes with high homology to IPP isomerase of *Saccharomyces cerevisiae*. It has been speculated that HMG-CoA reductase (Figure 1), which catalyzes the reaction from HMG-CoA to mevalonate, may be the rate limiting enzyme for terpenoids including carotenoids. However, as for IPP isomerase, any such report has not been presented. Therefore, increase of carotenoid production by introducing a IPP isomerase gene was a new finding.

The present invention provides a DNA chain having characteristics of increasing carotenoid production amount, and it containing the nucleotide sequence which encodes the polypeptide having the substantially same amino acid sequence as those of IPP isomerase, and a production method for carotenoid characterized by introducing said DNA chain into the carotenoid producing microorganism, culturing said transformed microorganism and increasing carotenoid content in the culture broth and cells.

The DNA chains of the present invention includes the DNA chains mentioned above (1) or (2), or the DNA chains which hybridize to said chains under stringent conditions.

Substantially, the polypeptides encoded by the DNA chains of the present invention have the amino acid sequences shown in SEQUENCE ID No. 1 (A-B in Figures 4 and 5) or in SEQUENCE ID No. 2 (C-D, in Figures 6 and 7). In the present invention, the polypeptides encoded by these DNA chains, the proteins of which amino acid sequence is substantially IPP isomerase, may be altered by deletion, replacement, addition and so forth of some amino acids, as long as the resulted polypeptides hold their higher carotenoid production activity. This allowance corresponds to "having the substantially same amino acid sequence substantially shown in SEQUENCE ID No. 1 or No. 2". As an example, a sequence which lacks the first amino acid (Met) can be included as the altered polypeptide or the altered enzyme. Needless to say, the DNA chains of the present invention include not only the chains having the nucleotide sequences which encode the amino acid sequences shown in SEQUENCE ID No. 1 and 2 (Figures 4 to 5), but also the degenerate isomers of the chains, which differs only on degenerate codons and encode the same polypeptides as the original chains do.

(1) Obtaining the DNA chains

One method to obtain a DNA chain having the nucleotide sequence which encodes the amino acid sequence of the above protein is chemical synthesis of the DNA chain at least a part of the chain according to the known nucleic acid synthesis method. However, considering that there are so many amino acids bound in the protein, it would be more preferable than chemical synthesis to make cDNA libraries of *Haematococcus pluvialis* or *Phaffia rhodozyma* or the like to obtain a targeted DNA chain by applying some popular method in the field of genetic engineering such as hybridization with appropriate probes.

(2) Transformation of microorganisms such as *E. coli* and expression of gene

Higher carotenoid content in culture broth or cells of microorganisms can be achieved by introducing the above mentioned DNA chain of the present invention into appropriate microorganisms such as carotenoid-producing bacteria such as *E. coli* and *Zymomonas mobilis* containing carotenoid biosynthesis genes from *Erwinia uredovora* and so forth, or carotenoid-producing yeast such as *Saccharomyces cerevisiae* containing carotenoid biosynthesis genes from *Erwinia uredovora* and so force.

The outline of the method to introduce exogenous genes into preferable microorganisms is mentioned below.

Procedures or methods to introduce and express exogenous genes in microorganisms such as *E. coli*, besides those mentioned below in the present invention, includes those widely used in the field of genetic engineering. Those are applicable to the invention. See "Vectors for cloning genes", Methods in Enzymology, 216: 469-631 (1992), Academic Press; "Other bacterial systems", Methods in Enzymology, 204: 305-636 (1991) Academic Press).

[*E. coli*]

There are some established and efficient methods to introduce exogenous genes to *E. coli* such as Hanahan's method and rubidium method, and they are applicable to the present invention (See Sambrook, J., Fritsch, E. F., Maniatis, T., "Molecular cloning-A laboratory manual", Cold Spring Harbor Laboratory Press (1989)). Expression of exogenous genes in *E. coli* can be performed by known methods. (See "Molecular cloning-A laboratory manual", *ibid.*), for example, vectors for *E. coli* such as pUC and pBluescript vectors having *lac* promoter can be used. The inventors of the present invention used pSPORT1 vector or pBluescript II KS vector having *lac* promoter as vectors for *E. coli*, and inserted the IPP isomerase gene, derived from *Haematococcus pluvialis*, *Phaffia rhodozyma* or *Saccharomyces cerevisiae*, into the *lac* promoter with the direction of reading through of the transcription, and expressed the gene in *E. coli*.

[Yeast]

There are some established methods such as the lithium method to introduce exogenous genes into *Saccharomyces cerevisiae*, yeast, and such methods are applicable to the present invention (See "New biotechnology on yeast", Ed. Bio-industry Association (Yuichi Akiyama, editor in chief, Igaku Syuppan Center). Expression of exogenous genes in yeast can be performed as follows. Using both promoters and terminators, e.g. for *PGK* and *GPD*, an expression-cassette is constructed by inserting the exogenous gene so that during transcription, the gene is to be read through at the position between the promoter and the terminator. Expression can be performed by inserting the expression cassette into a vector for *S. cerevisiae* such as YRp vectors (multi-copy vectors for yeast, replication starts at ARS sequence of yeast chromosome), YE_p vectors (multi-copy vectors for yeast, replication starts at 2 μ m DNA) and Ylp vectors (vectors for yeast chromosome, no starting point of replication in yeast) (See "New biotechnology on yeast", *ibid.*; "Genetic engineering for production of substances", Ed. Japanese Society of Agrochemical Chemistry, Asakura Publishing company; or Yamano, S., Ishii, T., Nakagawa, M., Ikenaga, H., Misawa, N., "Metabolic engineering for production of β -carotene and lycopene in *Saccharomyces cerevisiae*", Biosci. Biotech. Biochem., 58: 1112-1114 (1994)).

[*Zymomonas mobilis*]

Introduction of exogenous genes into *Zymomonas mobilis*, the ethanol-producing bacterium can be performed by conjugal transfer method which is commonly used for gram negative bacteria. Expression of exogenous gene in *Zymomonas mobilis* can be performed by using pZA22 vector for this bacterium (See Katsumi Nakamura, "Molecular breeding of *Zymomonas* bacteria", Journal of the Japanese Society of Agrochemical Chemistry, 63: 1016-1018 (1989); and Misawa, N., Yamano, S., Ikenaga, H., "Production of β -carotene in *Zymomonas mobilis* and *Agrobacterium tumefaciens* by introduction of the biosynthesis genes from *Erwinia uredovora*", Appl. Environ. Microbiol., 57: 1847-1849 (1991)).

(3) Method to increase carotenoid production in microorganisms

By applying the above mentioned procedures or methods for introduction and expression of exogenous genes in microorganisms, both the carotenoid synthesis genes and the IPP isomerase gene can be introduced to express, and microorganisms capable of producing large amount of carotenoid can be obtained.

Farnesyl pyrophosphate (FPP) is the common substrate not only for carotenoids but also for other terpenoids such as sesquiterpenes, triterpenes, sterols and hopanols. In general, since microorganisms are synthesizing terpenoids even though they are not capable of synthesizing carotenoids, basically all of the microorganisms possesses FPP as an intermediate metabolite. On the other hand, *Erwinia uredovora*, the non-photosynthetic bacterium having the carotenoid synthesis genes can synthesize up to several useful carotenoids such as lycopene, β -carotene, zeaxanthin by using FPP as a substrate. When the genes are combined with the carotenoid synthesis genes of *Agrobacterium aurantiacum*, the marine bacterium, up to several useful carotenoids such as cantaxanthin and astaxanthin can also be synthesized (See Figures 2 and 3). The inventors of the present invention already confirmed that by introducing *eri* genes of *Erwinia uredovora* into microorganisms such as *Saccharomyces cerevisiae*, yeast and *Zymomonas mobilis*, ethanol-producing bacteria; these microorganisms can produce carotenoids such as β -carotene as anticipated [Yamano, S., Ishii, T., Nakagawa, M., Ikenaga, H., Misawa, N., "Metabolic engineering for production of β -carotene and lycopene in *Saccharomyces cerevisiae*", Biosci. Biotech. Biochem., 58:1112-1114 (1994); Misawa, N., Yamano, S., Ikenaga, H., "Production of β -carotene in *Zymomonas mobilis* and *Agrobacterium tumefaciens* by introduction of the biosynthesis genes from *Erwinia uredovora*", Appl. Environ. Microbiol., 57:1847-1849 (1991); and Japanese laid-open Patent Application No. HEI 3-58786 (Japanese Patent Application filing No. HEI 2-53255): "A DNA chain useful for synthesis of carotenoids" by the inventors].

From the above findings, it can be expected that when an appropriate combinations of the carotenoid synthesis genes derived from *Er. uredovora* and those from marine bacteria (typically the carotenoid synthesis genes derived from

Ag. aurantiacum) are introduced into the same microorganism simultaneously, as a principle, all of the microorganisms, in which such genes are introduced and of which introduction-expression system is established, can produce useful carotenoids such as astaxanthin and zeaxanthin.

In such cases, if the IPP isomerase gene (typically, derived from Haematococcus pluvialis, Phaffia rhodozyma and Saccharomyces cerevisiae) is introduced according to the above mentioned method, and is expressed concomitantly with the above carotenoid synthesis gene, higher production amount of useful carotenoids can be achieved.

(4) Deposit of the microorganisms

The recombinant *E. coli* strain JM109 has been deposited as follows with the National Institute of Bioscience and Human-Technology, the Agency of Industrial Science and Technology. The strain contains the plasmid having the isolated gene which is the DNA chain of the invention. The names of the plasmids are shown in the parentheses.

(i) JM109(pRH1)

Deposit No.: FERM BP-5032

Date of Receipt: March 6th, 1995

(ii) JM109(pHP11)

Deposit No.: FERM BP-5031

Date of Receipt: March 6th, 1995

(ii) JM109(pSI1)

Deposit No.: FERM BP-5033

Date of Receipt: March 6th, 1995

BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1 shows the isoprene common biosynthetic pathway from HMG-CoA to FPP.

FIGURE 2 shows the carotenoid biosynthetic pathway, and the functions of the carotenoid synthesis genes of Erwinia uredovora, the non-photosynthetic bacterium.

FIGURE 3 shows the carotenoid biosynthetic pathway, and the functions of the carotenoid synthesis genes of Agrobacterium aurantiacum, the marine bacterium. The solid line shows major biosynthetic pathway and the dotted line shows minor one.

FIGURES 4 and 5 shows the nucleotide sequence of the IPP isomerase gene and the amino acid sequence of the polypeptide encoded by said gene of Phaffia rhodozyma, the astaxanthin-producing yeast. In the Figure, the sequence from mark A to B shows the open reading frame encoding the polypeptide consisting of 251 amino acids.

FIGURES 6 and 7 shows the nucleotide sequence of the IPP isomerase gene and the amino acid sequence of the polypeptide encoded by said gene of Haematococcus pluvialis, the astaxanthin-producing green alga. In the Figure, the sequence from mark C to D shows the open reading frame encoding the polypeptide consisting of 259 amino acids.

FIGURES 8 and 9 shows the nucleotide sequence of the IPP isomerase gene and the amino acid sequence of the polypeptide encoded by said gene of Saccharomyces cerevisiae, the yeast for laboratory use. In the Figure, the sequence from mark E to F shows the open reading frame encoding the polypeptide consisting of 288 amino acids.

FIGURE 10 shows the plasmids containing the carotenoid biosynthesis genes of Erwinia uredovora, the non-photosynthetic bacterium.

FIGURE 11 shows the plasmids containing the IPP isomerase gene of Phaffia rhodozyma, Haematococcus pluvialis, or Saccharomyces cerevisiae.

FIGURE 12 shows the growth curve in the culture broth of the lycopene producing *E. coli* strains(L:). In the Figure, "control" means the *E. coli* strain having no exogenous IPP isomerase gene.

FIGURE 13 shows the lycopene production curve in the culture broth of the lycopene producing *E. coli* strains(L:). In the Figure, "control" means the *E. coli* strain having no exogenous IPP isomerase gene.

FIGURE 14 shows production of lycopene(L:), β -carotene(β :) and phytoene(P:) in the cultured cells of the *E. coli* strains. In the Figure, "control" means the *E. coli* strain having no exogenous IPP isomerase gene.

EXAMPLE

The following examples illustrate the present invention in more detail, however, the present invention is not limited to them. The genetic recombination experiments used here are based on the standard methods(Sambrook, J., Fritsch, E. F., Maniatis, T., "Molecular cloning-A laboratory manual", Cold Spring Harbor Laboratory Press (1989)) unless otherwise stated.

(EXAMPLE 1) Biological materials and culture conditions

Phaffia rhodozyma ATCC 24230 Strain (Astaxanthin-producing yeast) registered at the American Type Culture Collection (ATCC) is used. YM media (yeast extract 0.3%, malt extract 0.3%, bacto-peptone 0.5%, Glucose 1%) is used for *Ph. rhodozyma*. *Haematococcus pluvialis*, the astaxanthin-producing green alga, NIES-144 strain registered at the Global Environmental Forum is used. *Ha. pluvialis* is cultured at 20°C for about 4 days in basic culture media (yeast extract 0.2%, sodium acetate 0.12%, L-asparagin 0.04%, magnesium chloride hexahydrate 0.02%, ferrous sulfate heptahydrate 0.001%, calcium chloride dihydrate 0.002%) under 12 hr light (20 $\mu\text{E}/\text{m}^2\text{s}$)/12 hr dark condition. Furthermore, in order to induce astaxanthin synthesis in *Ha. pluvialis*, cyst formation, a kind of differentiation, has to be induced. To induce cyst formation, both acetic acid 45 mM and ferrous sulfate heptahydrate 450 μM at final concentrations are added. *Ha. pluvialis* in the media is cultured for about 12 hr at 20°C with light (125 $\mu\text{E}/\text{m}^2\text{s}$). *Saccharomyces cerevisiae* (Yeast for laboratory use) S288C strain registered at the Yeast Genetic Stock Center is used. For *Sa. cerevisiae*, YPD media (yeast extract 1%, bacto-peptone 2%, glucose 2%) is used.

15 (EXAMPLE 2) Preparation of whole RNA in *Phaffia rhodozyma*

Phaffia rhodozyma ATCC-24230 strain is cultured with shaking for approx. 24 hr at 20°C in 400 ml of YM media. When the turbidity of the media reached at $\text{OD}_{600} = 0.4$, the bacteria are collected and frozen in liquid nitrogen. The frozen bacteria are stored in the freezer at -80°C and used for preparing total RNA. After thawing the frozen bacteria in a tube on ice, the bacteria are suspended in 6 ml of ANE buffer (10 mM-sodium acetate, 100 mM-sodium chloride, 1 mM EDTA, pH 6.0). Glass beads are added to cover the surface of the bacteria layer. Then, 600 μl of 10% SDS and 6 ml of phenol prewarmed at 65°C are added. The suspension is kept at 65°C for 5 minutes, and the tube is vortexed to crushed cell membranes at every 30 seconds. Then, the suspension is rapidly cooled down to room temperature and centrifuged for 10 minutes at 1,500 x g at room temperature. Equal volume of phenol is added to the supernatant and vortex for 2 minutes. Then the suspension was centrifuged for 10 minutes at 1,500 x g at room temperature. Then, by using equal volume of phenol/chloroform (1/1 (v/v)) and chloroform alone, the same procedures as above are performed. To the resulted supernatant, one tenth volume of 3 M sodium acetate and three volume of ethanol are added; then the supernatant is stored in the freezer at -20°C for 30 minutes. The supernatant is centrifuged for 15 minutes at 15,000 x g at 4°C, a pellet is rinsed with 70% ethanol and dried. The residual is dissolved in 200 μl of sterilized water to make total RNA solution of *Ph. rhodozyma*. By this preparation procedure, 1.6 mg of total RNA is obtained.

(EXAMPLE 3) Preparation of whole RNA in *Haematococcus pluvialis*

Haematococcus pluvialis NIES-144 strain is cultured for approx. 4 days in 800 ml of the basic culture media under the condition of 20°C, light intensity at 20 $\mu\text{E}/\text{m}^2\text{s}$ and 12 hr light/12 hr dark cycle. Then, both acetic acid 45 mM and ferrous sulfate heptahydrate 450 μM as final concentrations are added. The *H. pluvialis* in the media is cultured for approx. 12 hr at 20°C with light (125 $\mu\text{E}/\text{m}^2\text{s}$). The bacteria are collected from the media, frozen in liquid nitrogen and crushed in the mortar to give powder. Then, three ml of ISOGEN-LS [Nippon-Gene K.K.] is added to the powder and stand for 5 minutes. Then 0.8 ml of chloroform is added, and the solution is stirred vigorously for 15 seconds and stand at room temperature for 3 minutes. The solution is centrifuged for 15 minutes at 4°C, 12,000 x g, two ml of isopropanol is added to the supernatant and the supernatant is stood at room temperature for 10 minutes. Then, the solution is centrifuged for 10 minutes at 4°C, 12,000 x g. The resulted pellet is rinsed with 70% ethanol to dry. After drying, the residual is dissolved in 1 ml of TE buffer (10 mM Tris-HCl pH 8.0, 1 mM EDTA) to make total RNA solution of *Ha. pluvialis*. By this preparation procedure, 4.1 mg of whole RNA was obtained.

45 (EXAMPLE 4) Establishing cDNA expression libraries of *Phaffia rhodozyma* and *Haematococcus pluvialis*

By using Oligotex-dT30 Super [Takara Syuzo K.K.], poly A + RNA from *Phaffia rhodozyma* and *Haematococcus pluvialis* are purified from approx. 1 mg total RNA respectively. The purification is performed according to the methods mentioned in the package insert. By following the method, approx. 26 μg of poly A + mRNA from *Ph. rhodozyma* and approx. 14 μg of it from *Ha. pluvialis* are purified.

Preparation of cDNA is performed with Superscript™ plasmid system (GIBCO BRL) by the method mentioned in the package insert with some modifications. Approx. 5 μg of poly A + mRNA is used. A synthetic DNA consisting of the recognition sequence for the restriction enzyme *NotI* and 15 mers oligo-dT is used as a primer. The complementary DNA is synthesized with reverse transcriptase, SUPERScript RT. Then, by using *Escherichia coli* DNA ligase, *E. coli* DNA polymerase and *E. coli* RNase H, double strand DNA is synthesized. Then, the linker of the restriction enzyme *Sall* is bound by using T4 DNA ligase. cDNA is designed to have the *Sall*-site at the upstream terminal of itself and the *NotI* site at the downstream of poly A. Fractionation by size of these cDNAs is performed by electrophoresis and the fractions ranging from 0.7 kb to 3.5 kb are collected. cDNA in the collected fractions is ligated to cDNA expression vector

pSPORT I NotI-Sall-Cut by using both the ligation buffer which is included in the kit, 50 mM Tris-HCl pH 7.6, 10 mM MgCl₂, 1 mM ATP, 1 mM DTT, 5% PEG 8,000 and T4 DNA Ligase. The cDNA expression vector pSPORT I has lac promoter at the upstream of the Sall site and can express cDNA in *E. coli*. Then, by using whole the ligated DNA solution, transformation of the competent cells of *E. coli* DH5 α prepared is performed according to the method described in "Molecular Cloning 2nd edition: Cold Spring Harbor Laboratory, 1.21-1.41(1989). Approx. 200,000 transformed strains of *Ph. rhodozyma* and approx. 40,000 transformed strains of *Ha. pluvialis* are obtained. After collecting all of the transformants, the plasmid DNA is prepared according to the method described in "Molecular Cloning 2nd edition, *ibid.*" As a result, 0.9 mg and 0.6 mg of plasmid DNAs are obtained respectively and these are assigned as cDNA libraries of *Ph. rhodozyma* and *Ha. pluvialis*.

(EXAMPLE 5) Preparation of carotenoid-producing *E. coli*

The plasmid pCAR16(Misawa, N., Nakagawa, M., Kobayashi, K., Yamano, S., Izawa, Y., Nakamura, K., Harashima, K., "Elucidation of the *Erwinia uredovora* carotenoid biosynthetic pathway by functional analysis of gene products expressed in *Escherichia coli*", J. Bacteriol., 172:p.6704-6712 (1990) and Japanese Patent Application laid-open No. HEI 3-58786 (Japanese Patent Application filing No. HEI 2-53255): "A DNA chain useful for synthesis of carotenoids" by the present inventors) having the carotenoid synthesis genes except for crtZ derived from *Erwinia uredovora*, is digested with BstEII, treated with Klenow enzyme and religated to inactivate the crtX gene by frame shift. After that, the 6.0 kb Asp718(KpnI)-EcoRI fragment containing crtE, crtB, crtI and crtY genes necessary for β -carotene production is taken out. The fragment is then inserted into the EcoRV sites of the *E. coli* vector pACYC184 and the desirable plasmid(named pACCAR16 Δ crtX, FIGURE 10) is obtained. *E. coli* containing this plasmid (pACCAR16 Δ crtX) is chloramphenicol resistant and has yellowish color due to β -carotene production.

Then, the plasmid pCAR16 is digested with BstEII/SnaBI, treated with Klenow enzyme and religated to remove the 2.26 kb BstEII-SnaBI fragment containing crtX and crtY genes. After that, the 3.75 kb Asp718(KpnI)-EcoRI fragment containing crtE, crtB and crtI genes necessary for lycopene production is taken out. The fragment is then inserted into the EcoRV sites of the *E. coli* vector pACYC184 and the desirable plasmid(named pACCRT-EIB, FIGURE 10) is obtained. *E. coli* containing pACCRT-EIB is chloramphenicol resistant and has reddish color due to lycopene production (Cunningham Jr., F. X., Chamovitz, D., Misawa, N., Gatt, E., Hirschberg, J., "Cloning and functional expression in *Escherichia coli* of a cyanobacterial gene for lycopene cyclase, the enzyme that catalyzes the biosynthesis of β -carotene", FEBS Lett., 328: 130-138 (1993)).

Then, the plasmid pCAR16 is digested with BstEII/Eco52I, treated with Klenow enzyme and religated to remove the 3.7 kb BstEII-Eco52I fragment containing crtX, crtY and crtI genes. After that, the 2.3 kb Asp718(KpnI)-EcoRI fragment containing crtE and crtB genes(FIGURE 2) necessary for phytoene production is taken out. The fragment is then inserted into the EcoRV sites of the *E. coli* vector pACYC184 and the desirable plasmid(named pACCRT-EB, FIGURE 10) is obtained. *E. coli* containing pACCRT-EB is chloramphenicol resistant and does not show color change as phytoene is colorless (Linden, H., Misawa, N., Chamovitz, D., Pecker, I., Hirschberg, J., Sandmann, G., "Functional complementation in *Escherichia coli* of different phytoene desaturase genes and analysis of accumulated carotenes", Z. Naturforsch. 46c: 1045-1051 (1991)).

(EXAMPLE 6) Screening of genes that increase β -carotene production

As the *E. coli* strain JM101 containing the above plasmid pACCAR16 Δ crtX shows yellowish color due to β -carotene production, it was investigated whether more yellowish transformant can be obtained by introducing cDNA expression library of *Phaffia rhodozyma* or *Haematococcus pluvialis*. As a first step, competent cells of *E. coli* JM101 containing pACCAR16 Δ crtX are prepared according to the method described in "Molecular cloning 2nd edition: Cold Spring Harbor Laboratory, 1.21-1.41(1989). Then, one hundred ng of each cDNA expression library of *Ph. rhodozyma* and *Ha. pluvialis* is introduced to 1 ml of the competent cells. Approx. 200,000 transformants of *Ph. rhodozyma* and approx. 40,000 transformants of *Ha. pluvialis* are obtained and inoculated for screening on the LB plate(bactotrypton 1%, yeast extract 0.5%, NaCl 1%, agar 1.5%) containing 150 μ g/ml of ampicillin, 30 μ g/ml of chloramphenicol and 1 mM of IPTG. From the screening, 5 strains of *Ph. rhodozyma* and 10 strains of *Ha. pluvialis* shows deep yellowish color than other strains and they are isolated. The plasmid DNA extracted from these strains is subject to restriction enzyme analysis, and it was found that the plasmids from the five strains and ten strains have common DNA fragment respectively. Of these screened plasmids derived from the cDNA expression libraries, a plasmid from *Ph. rhodozyma* was named pRH1(Figure 11) and another plasmid from *Ha. pluvialis* was named pHP1. In addition to that, a fragment is taken out after digesting pHP1 with Sall and NotI, and then, the fragment is inserted into pBluescript KS+. The resulted plasmid was named pHP11(FIGURE 11) and was used for the experiments mentioned below.

(EXAMPLE 7) Nucleotide sequence determination on the gene that increases β -carotene production

From the plasmids pRH1 and pHP1, the deletion plasmids which lack various lengths from the original plasmids are prepared by the following procedures. By using those deletion plasmids, the nucleotide sequences are determined. Decomposition of pRP1 is performed with both *EcoRI* and *PstI*, or with both *NcoI* and *SphI*. Decomposition of pHP1 is performed with both *AatII* and *BamHI*, or with both *KpnI* and *EcoRI*. After extraction with phenol/chloroform, DNA is recovered by ethanol precipitation. Each DNA fraction is then dissolved in 100 μ l portions of ExoIII buffer (50mM Tris-HCl, 100mM NaCl, 5mM MgCl₂, 10mM 2-mercaptoethanol, pH 8.0) and is kept at 37°C after addition of 180 units of ExoIII nuclease. Ten μ l portions of the solution are sampled every 30 seconds and transferred to tubes containing 10 μ l of MB buffer (40 mM NaCl, 2 mM ZnCl₂, 10% glycerol, pH 4.5) in an ice bath. After sampling, the 10 tubes are kept at 65°C for 10 minutes to inactivate the enzyme. Then, 5 units of mung bean nuclease is added and kept at 37°C for 30 minutes. From one original plasmid, ten different kind of DNA fragments are recovered by agarose gel electrophoresis. The degree of deletion of each fragment varies. The terminals of the recovered DNAs are smoothed with Klenow enzyme to subject to ligation reaction at 16°C overnight, and by using resulting DNA, *E. coli* DH5 α is transformed to obtain clones. The plasmids are prepared from the various clones obtained, and nucleotide sequences are determined by using luminescence primer cycle sequence kit (Applied Biosystems corp.) with an automatic sequencer.

As a result, it was found that the nucleotide sequence of the cDNA in pRH1 derived from *Phaffia rhodozyma* consists of 1,099 base pairs (SEQUENCE ID No. 4), and there is an open reading frame which encodes a polypeptide having 251 amino acids (which corresponds the region from A to B in Figures 4 and 5). It was also found that the nucleotide sequence of the cDNA in pHP1 derived from *Haematococcus pluvialis* consists of 1,074 base pairs (SEQUENCE ID No. 5), and there is an open reading frame which encodes a polypeptide having 259 amino acids (which corresponds the region from C to D in Figures 6 and 7). The amino acid sequences expected from these open reading frames are investigated by analyzing homology in the Gene Bank. Both of the amino acid sequences of *Ph. rhodozyma* and *Ha. pluvialis* have significant homology with the IPP isomerase gene of *Saccharomyces cerevisiae*, 27.0% for *Ph. rhodozyma* and 20.3% for *Ha. pluvialis*. Therefore the genes were identified as the IPP isomerase gene.

(EXAMPLE 8) Preparation of total DNA in *Saccharomyces cerevisiae*

Preparation of total DNA in *Saccharomyces cerevisiae* is performed according to the method described in "Methods in Yeast Genetics; a laboratory course manual: Cold Spring Harbor Laboratory, p.131-132(1990). *S. cerevisiae* S288C strain is inoculated in 10 ml of YPD media and cultured at 30°C overnight. The cultured cells are collected and suspended in 0.5 ml of sterilized water for washing. By discarding the supernatant, the yeast are collected again. A 0.2 ml of the mixture (2% Triton X-100, 1% SDS, 100 mM NaCl, 10 mM Tris-HCl(pH 8), 1mM EDTA), 0.2 ml of phenol/chloroform/isoamylalcohol (25/24/1 (v/v/v)) and 0.3 g of glass beads are added. After vortex mix for 3-4 minutes, two hundred μ l of TE buffer (10 mM Tris-HCl(pH 8), 1 mM EDTA) is added. Then the solution is centrifuged for 5 minutes, and the supernatant is transferred to another tube and 1 ml of ethanol is added. Then the solution is centrifuged again for 2 minutes. The resulted pellet is dissolved in 0.4 ml of TE buffer. Then, two μ l of RNase A (10 mg/ml) is added and the solution is stood for 5 minutes at 37°C. Then, ten μ l of 4 M ammonium acetate and 1 ml of ethanol are added. After mixing well, the solution is centrifuged for 2 minutes and the resulted pellet is recovered. After drying the pellet, it was dissolved with 50 μ l of TE buffer to have total DNA of *S. cerevisiae* S288C strain. By this preparation procedure, 3.4 μ g of total DNA was obtained.

(EXAMPLE 9) Isolation of the IPP isomerase gene of *Saccharomyces cerevisiae* by PCR method

Based on the nucleotide sequence of the IPP isomerase gene of *S. cerevisiae* reported in the aforementioned reference (Anderson, M. S., Muehlbacher, M., Street, I.P., Proffitt, J., Poulter, C. D., "Isopentenyl diphosphate: dimethylallyl diphosphate isomerase - an improved purification of the enzyme and isolation of the gene from *Saccharomyces cerevisiae*", J. Biol. Chem., 264:19169-19175(1989)), the primers below were synthesized.

Primer No. 1 5'-TCGATGGGGGTTGCCTTTCTTTTTCGG-3'

Primer No. 2 5'-CGGGTTGTTATAGCATCTATGAATTTGCC-3'

The procedure was designed to obtain PCR amplified IPP isomerase gene having *TagI* sites at the upstream terminal and *AccII* region at the downstream terminal. Thirty cycles of PCR is performed with 200 ng of total DNA of *S. cerevisiae* and PfuDNA polymerase (STRATAGENE). To express the IPP isomerase gene obtained by PCR in *E. coli*, it is digested with both *TagI* and *AccII*. Then, the gene was inserted into *ClaI* sites and *SmaI* sites of pBluescript KS+ vector. The resulted plasmid was named pSI1 (Figure 11). This DNA derived from *S. cerevisiae* had a nucleotide sequence consisting of 1,058 bp (SEQUENCE ID No. 6), and contained a gene which encodes IPP isomerase consisting of 288 amino acids (corresponds from E to F in Figures 8 and 9).

(EXAMPLE 10) Increase of lycopene production amount by introducing the IPP isomerase gene

Into the lycopene-producing *E. coli* JM101 strain (abbreviated as L hereafter) which contains pACCRT-EIB(Figure 10), pSPORT1 vector, pRH1 plasmid containing the IPP isomerase gene of *Phaffia rhodozyma*, PHP11 plasmid containing the IPP isomerase gene of *Haematococcus pluvialis* or pSI1 plasmid containing the IPP isomerase gene of *Saccharomyces cerevisiae*(FIGURE 11) are introduced respectively. These *E. coli* transformants are then plated on the LB plate containing 150 µg/ml of ampicillin(Ap), 30 µg/ml of chloramphenicol(Cm) and 1 mM of IPTG, and cultured at 28°C overnight. The three strains, in which each IPP isomerase gene were introduced, showed deep reddish color due to lycopene production compared with the control (lycopene-producing *E. coli*) in which only vector is introduced. Furthermore, growth rate of the three strains on agar plates were faster than the control strains and they always showed larger colonies than those of the control during culture. It is considered that due to introduction and expression of the IPP isomerase gene, the upstream of the biosynthetic pathway up to FPP became more efficient(see FIGURE 1), and consequently, increase of FPP supply led to increase of lycopene. As for faster growth rate, it is also considered that due to increase of FPP, sufficient amount of the substrate can be supplied not only for lycopene production but also for the production of other membrane components derived from FPP, that is, FPP or GGPP binding protein, and these components are necessary for growth of *E. coli*.

Increase of lycopene production amount by *E. coli* carrying the IPP isomerase gene is also confirmed by liquid culture. After overnight shaking culture of the LB media(5 ml) containing both Ap and Cm at 28°C, 2 ml of the media is taken and transferred to 200 ml of 2YT culture media(1.6% bactotrypton, 1% yeast extract, 0.5% NaCl) containing Ap, Cp and 0.1 mM IPTG, and shaking culture is performed at 230 rpm, 28°C. Five ml each of the media is sampled several hours' intervals to determine growth rate and lycopene content. Growth rate is calculated from absorbance at 650 nm. Lycopene content is determined according to the following procedure. The cells collected by centrifugation, 2.5 ml of acetone is added to the cells and stand for 30 minutes. Vortex mix once in a while. After filtration, absorbance at 474 nm is measured to determine the lycopene content based on the absorbance 185.0 for 1 mM lycopene (light path: 1 cm). JASCO UVIDEC-220B spectrophotometer is used. By using HPLC, it is confirmed that these strains actually produced lycopene and absorbance at 474 nm is attributable to lycopene. HPLC conditions are mentioned in EXAMPLE 11. The results are shown in Figure 12(growth curve) and Figure 13(lycopene production curve). As for the growth rate(Figure 12), there is no difference among any the strains including the control strains. This result is different from that obtained from culture plates. Probably, when the liquid culture is performed, even in the control strain which does not have exogenous IPP isomerase gene can grow rapidly, because the supply of the substrate for membrane components such as FPP and GGPP binding protein is enough compared to agar culture is done. In contrast, there is a big difference between the control strain having no exogenous IPP isomerase gene and the three exogenous IPP isomerase gene-carrying strains. During culture, the three strains always showed several times higher lycopene production amount compared with the control strain. Lycopene production amount per *E. coli* dry weight at 28 hr after the start of the culture is shown in Figure 14. The three strains containing the IPP isomerase gene showed 3.6-4.5 times higher production than the control strain. Lycopene-producing *E. coli* containing PHP11 is able to produce 1.03 mg lycopene per 1g dry weight.

(EXAMPLE 11) Increase of β-carotene production amount by introducing the IPP isomerase gene

Into the β-carotene producing *E. coli* JM101 strain (abbreviated as β hereafter) which contains pACCAR16ΔcrX(FIGURE 10), either pSPORT1 vector or pRH1 plasmid containing the IPP isomerase gene of *Phaffia rhodozyma* is introduced separately. After overnight shaking culture of the LB media(5 ml) containing both Ap and Cm at 28°C, 1 ml of the media is taken and transferred to 100 ml of 2YT media containing Ap, Cm and 0.1 mM IPTG, and shaking culture is performed at 230 rpm at 28°C for 28 hr. The bacteria are collected by centrifugation and washed with 0.85% NaCl. After washing, the bacteria are suspended in 40 ml of acetone and allowed to stand for 30 minutes. Vortex mix once in a while. After filtration, absorbance at 454 nm is measured to determine β-carotene content based on the absorbance 134.4 for 1 mM β-carotene (light path: 1 cm). The result is shown in FIGURE 14. β-Carotene producing *E. coli* containing pRH1 produced 709 µg of β-carotene per 1g dry weight. This amount is 1.5 times higher than the control.

By using HPLC on the above acetone extract, it is confirmed that these strains actually produced β-carotene and absorbance at 454 nm is attributable to β-carotene. Novapack HR 6µ C18(3.9 x 300 mm, Waters) is used as a column. Acetonitrile/methanol/2-propanol(90/6/4(v/v/v)) is used as an elution solvent. A photodiode array detector 996(Waters) is used to monitor an elution profile. The results showed that almost 100% of a peak appeared in a visible spectrum is β-carotene. As the β-carotene standard preparation, chemically synthesized β-carotene (Sigma) is used.

(EXAMPLE 12) Increase of phytoene production amount by introducing the IPP isomerase gene

Into the phytoene producing *E. coli* JM101 strain (abbreviated as P hereafter) which contains pACCRT-EB(FIGURE 10), any of pSPORT1 vector, pRH1 plasmid containing the IPP isomerase gene of *Phaffia rhodozyma* or PHP11 plas-

mid-containing the IPP isomerase gene of *Haematococcus pluvialis* is introduced separately. After overnight shaking culture of the LB media(5 ml) containing both Ap and Cm at 28°C, 1 ml of the media is taken and transferred to 100 ml of 2YT media containing Ap, Cm and 0.1 mM IPTG, and shaking culture is performed at 230 rpm at 28°C for 28 hr. The bacteria are collected by centrifugation and washed with 0.85% NaCl. After washing, the bacteria are suspended in 40 ml of acetone and allowed to stand for 30 minutes. Vortex mix once in a while. After filtration and drying by rotary evaporator, partition is performed with 40 ml of petroleum ether and water. Absorbance of the ether layer at 286 nm is measured to determine phytoene content based on the absorbance 41.2 for 1 mM phytoene (light path: 1 cm). As HPLC analysis described in EXAMPLE 11 showed that 70% of the absorbance at 286 nm is attributable to phytoene, an and also actual phytoene content is adjusted to 70% of the above value. The result is shown in FIGURE 14. Phytoene-producing *E. coli* containing the IPP isomerase gene produced 1.7-2.1 times higher phytoene than control strain.

From the above examples, we showed that by introducing the IPP isomerase gene into β -carotene, lycopene or phytoene-producing *E. coli*, several times higher carotenoid production is actually achieved. It is considered that due to introduction and expression of the IPP isomerase gene, upstream of the biosynthetic pathway up to FPP became more efficient(see FIGURE 1), and consequently, increase of FPP supply led to increase of these carotenoids. Therefore, it is considered that this findings can be applicable not only for β -carotene, lycopene and phytoene productions but also for all other carotenoids such as astaxanthin and zeaxanthin.

The present invention provides a DNA chain which can significantly increase carotenoid production in biosynthesis of carotenoid by microorganisms and a method to obtain several times higher carotenoid production amount by introducing and expressing said DNA chain into carotenoid-producing microorganisms. It is expected that said DNA chain can be applicable to increase production in microorganisms not only for carotenoids but also for terpenoids and so forth which require same substrate(FPP) as carotenoids.

[SEQUENCE LISTING]

SEQUENCE ID No.: 1

LENGTH: 251

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: peptide

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 20 25 30
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 35 40 45
 Lys Lys Thr Cys His Leu Met Ser Asp Ile Asn Ala Pro Lys Asp Leu
 50 55 60
 Leu His Arg Ala Phe Ser Val Phe Leu Phe Arg Pro Ser Asp Gly Ala
 65 70 75 80
 Leu Leu Leu Gln Arg Arg Ala Asp Glu Lys Ile Thr Phe Pro Gly Met
 85 90 95
 Trp Thr Asn Thr Cys Cys Ser His Pro Leu Ser Ile Lys Gly Glu Val
 100 105 110
 Glu Glu Glu Asn Gln Ile Gly Val Arg Arg Ala Ala Ser Arg Lys Leu
 115 120 125
 Glu His Glu Leu Gly Val Pro Thr Ser Ser Thr Pro Pro Asp Ser Phe
 130 135 140
 Thr Tyr Leu Thr Arg Ile His Tyr Leu Ala Pro Ser Asp Gly Leu Trp
 145 150 155 160
 Gly Glu His Glu Ile Asp Tyr Ile Leu Phe Ser Thr Thr Pro Thr Glu
 165 170 175
 His Thr Gly Asn Pro Asn Glu Val Ser Asp Thr Arg Tyr Val Thr Lys
 180 185 190
 Pro Glu Leu Gln Ala Met Phe Glu Asp Glu Ser Asn Ser Phe Thr Pro
 195 200 205
 Trp Phe Lys Leu Ile Ala Arg Asp Phe Leu Phe Gly Trp Trp Asp Gln
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 225 230 235 240

Glu Asp Leu Ser Asp Asn Lys Val Trp Lys Met ***

245

250

SEQUENCE ID No.: 2

LENGTH: 259

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: peptide

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 35 40 45
 Leu Glu Cys His Lys Phe Leu Pro His Gln Pro Ala Gly Leu Leu His
 50 55 60
 Arg Ala Phe Ser Val Phe Leu Phe Asp Asp Gln Gly Arg Leu Leu Leu
 65 70 75 80
 Gln Gln Arg Ala Arg Ser Lys Ile Thr Phe Pro Ser Val Trp Thr Asn
 85 90 95
 Thr Cys Cys Ser His Pro Leu His Gly Gln Thr Pro Asp Glu Val Asp
 100 105 110
 Gln Leu Ser Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys Ala Ala
 115 120 125
 Ala Ile Arg Lys Leu Glu His Glu Leu Gly Ile Pro Ala His Gln Leu
 130 135 140
 Pro Ala Ser Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys Ala Ala
 145 150 155 160
 Asp Val Gln Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu His Glu
 165 170 175
 Met Asp Tyr Ile Leu Phe Ile Arg Ala Asn Val Thr Leu Ala Pro Asn
 180 185 190
 Pro Asp Glu Val Asp Glu Val Arg Tyr Val Thr Gln Glu Glu Leu Arg
 195 200 205

Gln Met Met Gln Pro Asp Asn Gly Leu Gln Trp Ser Pro Trp Phe Arg
 210 215 220
 5 Ile Ile Ala Ala Arg Phe Leu Glu Arg Trp Trp Ala Asp Leu Asp Ala
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 Ala Leu Asn Thr Asp Lys His Glu Asp Trp Gly Thr Val His His Ile
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 10 Asn Glu Ala ***

15 SEQUENCE ID No.: 3

LENGTH: 288

SEQUENCE TYPE: amino acid

20 TOPOLOGY: linear

MOLECULAR TYPE: peptide

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 35 40 45
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 50 55 60
 35 Glu Gln Ile Lys Leu Met Asn Glu Asn Cys Ile Val Leu Asp Trp Asp
 65 70 75 80
 Asp Asn Ala Ile Gly Ala Gly Thr Lys Lys Val Cys His Leu Met Glu
 85 90 95
 40 Asn Ile Glu Lys Gly Leu Leu His Arg Ala Phe Ser Val Phe Ile Phe
 100 105 110
 Asn Glu Gln Gly Glu Leu Leu Leu Gln Gln Arg Ala Thr Glu Lys Ile
 115 120 125
 45 Thr Phe Pro Asp Leu Trp Thr Asn Thr Cys Cys Ser His Pro Leu Cys
 130 135 140
 Ile Asp Asp Glu Leu Gly Leu Lys Gly Lys Leu Asp Asp Lys Ile Lys
 50 145 150 155 160
 Gly Ala Ile Thr Ala Ala Val Arg Lys Leu Asp His Glu Leu Gly Ile

165 170 175
 Pro Glu Asp Glu Thr Lys Thr Arg Gly Lys Phe His Phe Leu Asn Arg
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 195 200 205
 Asp Tyr Ile Leu Phe Tyr Lys Ile Asn Ala Lys Glu Asn Leu Thr Val
 10 210 215 220
 Asn Pro Asn Val Asn Glu Val Arg Asp Phe Lys Trp Val Ser Pro Asn
 225 230 235 240
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 15 245 250 255
 Phe Lys Ile Ile Cys Glu Asn Tyr Leu Phe Asn Trp Trp Glu Gln Leu
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SEQUENCE ID No.: 4

LENGTH: 1099

SEQUENCE TYPE: nucleic acid

STRANDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: cDNA

ORIGIN

ORGANISM: Phaffia rhodozyma

STRAIN: ATCC 24230

SEQUENCE CHARACTERISTIC

CHARACTERISTIC CODE: CDS

LOCATION: 99..851

DETERMINATION METHOD: E

SEQUENCE:

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AACCGAAAAG AAAGAAGGCA GAGGAAAATA TATTCTAG ATG TCC ATG CCC AAC ATT 116

Met Ser Met Pro Asn Ile

5

GTT CCC CCC GCC GAG GTC CGA ACC GAA GGA CTC AGT TTA GAA GAG TAC 164

Val Pro Pro Ala Glu Val Arg Thr Glu Gly Leu Ser Leu Glu Glu Tyr

10

15

20

GAT GAG GAG CAG GTC AGG CTG ATG GAG GAG CGA TGT ATT CTT GTT AAC 212

Asp Glu Glu Gln Val Arg Leu Met Glu Glu Arg Cys Ile Leu Val Asn

25

30

35

CCG GAC GAT GTG GCC TAT GGA GAG GCT TCG AAA AAG ACC TGC CAC TTG 260

Pro Asp Asp Val Ala Tyr Gly Glu Ala Ser Lys Lys Thr Cys His Leu

40

45

50

ATG TCC AAC ATC AAC GCG CCC AAG GAC CTC CTC CAC CGA GCA TTC TCC 308

Met Ser Asn Ile Asn Ala Pro Lys Asp Leu Leu His Arg Ala Phe Ser

55

60

65

70

GTG TTT CTC TTC CGC CCA TCG GAC GGA GCA CTC CTG CTT CAG CGA AGA 356

Val Phe Leu Phe Arg Pro Ser Asp Gly Ala Leu Leu Leu Gln Arg Arg

75

80

85

GCG GAC GAG AAG ATT ACG TTC CCT GGA ATG TGG ACC AAC ACG TGT TGC 404

Ala Asp Glu Lys Ile Thr Phe Pro Gly Met Trp Thr Asn Thr Cys Cys

90

95

100

AGT CAT CCT TTG AGC ATC AAG GGC GAG GTT GAA GAG GAG AAC CAG ATC 452

Ser His Pro Leu Ser Ile Lys Gly Glu Val Glu Glu Glu Asn Gln Ile

105

110

115

GGT GTT CGA CGA GCT GCG TCC CGA AAG TTG GAG CAC GAG CTT GGC GTG 500

Gly Val Arg Arg Ala Ala Ser Arg Lys Leu Glu His Glu Leu Gly Val

120

125

130

CCT ACA TCG TCG ACT CCG CCC GAC TCG TTC ACC TAC CTC ACT AGG ATA 548

Pro Thr Ser Ser Thr Pro Pro Asp Ser Phe Thr Tyr Leu Thr Arg Ile

135

140

145

150

CAT TAC CTC GCT CCG AGT GAC GGA CTC TGG GGA GAA CAC GAG ATC GAC 596

His Tyr Leu Ala Pro Ser Asp Gly Leu Trp Gly Glu His Glu Ile Asp

155

160

165

TAC ATT CTC TTC TCA ACC ACA CCT ACA GAA CAC ACT GGA AAC CCT AAC 644

Tyr Ile Leu Phe Ser Thr Thr Pro Thr Glu His Thr Gly Asn Pro Asn

170

175

180

GAA GTC TCT GAC ACT CGA TAT GTC ACC AAG CCC GAG CTC CAG GCG ATG 692

Glu Val Ser Asp Thr Arg Tyr Val Thr Lys Pro Glu Leu Gln Ala Met

55

```

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5  Phe Glu Asp Glu Ser Asn Ser Phe Thr Pro Trp Phe Lys Leu Ile Ala
      200              205              210
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Arg Asp Phe Leu Phe Gly Trp Trp Asp Gln Leu Leu Ala Arg Arg Asn
10 215              220              225              230
GAA AAG GGT GAG GTC GAT GCC AAA TGG TTG GAG GAT CTC TCG GAC AAC 836
Glu Lys Gly Glu Val Asp Ala Lys Ser Leu Glu Asp Leu Ser Asp Asn
      235              240              245
15 AAA GTC TGG AAG ATG TAGTCGACC CTTCTTTCTG TACAGTCATC TCAGTTGGCC 890
Lys Val Trp Lys Met ***
      250
20 TGTTGGTTGC TTGCTTCTTG CTCTTCTTTC TATATATCTT TTTTCTTGCC TGGGTAGACT 950
TGATCTTTCT ACATAGCATA CGCATACATA CATAAACTCT ATTTCTTGTT CTTTATCTCT 1010
25 CTTCTAAGGG AATCTTCAAG ATCAATTCT TTTTGGGCTA CAACATTTC AATCAATGTT 1070
GCTTTTCAGA CTACAAAAAA AAAAAAAA 1099

```

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30
35 SEQUENCE ID No.: 5
    LENGTH: 1074
    SEQUENCE TYPE: nucleic acid
40 STRANDNESS: double
    TOPOLOGY: linear
    MOLECULAR TYPE: cDNA
45 ORIGIN
    ORGANISM: Haematococcus pluvialis
    STRAIN: NIES-144
50 SEQUENCE CHARACTERISTIC
55

```

CHARACTERISTIC CODE: CDS

LOCATION: 145..921

DETERMINATION METHOD: E

SEQUENCE:

ATCGCTACTT GGAACCTGGC CCGGCGGCAG TCCGATGACG CGATGCTTCG TTCGTTGCTC 60
 AGAGGCCTCA CGCATTTCCT CCGCGTGAAC TCCGCGCAGC AGGCCAGCTG TGCACACGEG 120
 CGACTCCAGT TTAGGCCAG AAGC ATG CAG CTG CTT GCC GAG GAC CGC ACA GAC 170
 Met Gln Leu Leu Ala Glu Asp Arg Thr Asp
 CAT ATG AGG GGT GCA AGT ACC TGG GCA GGC GGG CAG TCG CAG GAT GAG 222
 His Met Arg Gly Ala Ser Thr Trp Ala Gly Gly Gln Ser Gln Asp Glu
 CTG ATG CTG AAG GAC GAG TGC ATC TTG GTG GAT GCT GAC GAC AAC ATT 270
 Leu Met Leu Lys Asp Glu Cys Ile Leu Val Asp Ala Asp Asp Asn Ile
 ACA GGC CAT GTC AGC AAG CTG GAG TGC CAC AAG TTC CTA CCA CAT CAG 318
 Thr Gly His Val Ser Lys Leu Glu Cys His Lys Phe Leu Pro His Gln
 CCT GCA GGC CTG CTG CAC CGG GCC TTC TCT GTA TTC CTG TTT GAC GAC 366
 Pro Ala Gly Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asp Asp
 CAG GGG CGA CTG CTG CTG CAA CAG CGT GCA CGA TCA AAA ATC ACA TTC 414
 Gln Gly Arg Leu Leu Leu Gln Gln Arg Ala Arg Ser Lys Ile Thr Phe
 CCC AGT GTG TGG ACC AAC ACC TGC TGC AGC CAC CCT CTA CAT GGG CAG 462
 Pro Ser Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu His Gly Gln
 ACC CCA GAT GAG GTG GAC CAA CTA AGC CAG GTG GCC GAC GGC ACA GTA 510
 Thr Pro Asp Glu Val Asp Gln Leu Ser Gln Val Ala Asp Gly Thr Val
 CCT GGC GCA AAG GCT GCT GCC ATC CGC AAG TTG GAG CAC GAG CTG GGG 558
 Pro Gly Ala Lys Ala Ala Ala Ile Arg Lys Leu Glu His Glu Leu Gly
 ATA CCA GCG CAC CAG CTG CCG GCC AGC GCG TTT CGC TTC CTC ACG CGT 606
 Ile Pro Ala His Gln Leu Pro Ala Ser Ala Phe Arg Phe Leu Thr Arg

TTG CAC TAC TGC GCC GCG GAC GTG CAG CCG GCT GGG ACA CAA TCA GCA 654
 Leu His Tyr Cys Ala Ala Asp Val Gln Pro Ala Ala Thr Gln Ser Ala
 155 160 165 170
 CTC TGG GGC GAG CAC GAA ATG GAC TAC ATC TTA TTC ATC CGG GCC AAC 702
 Leu Trp Gly Glu His Glu Met Asp Tyr Ile Leu Phe Ile Arg Ala Asn
 175 180 185
 GTC ACC CTT GCG CCC AAC CCT GAC GAG GTG GAC GAA GTC AGG TAC GTG 750
 Val Thr Leu Ala Pro Asn Pro Asp Glu Val Asp Glu Val Arg Tyr Val
 190 195 200
 ACG CAG GAG GAG CTG GCG CAG ATG ATG CAG CCG GAC AAT GGG TTG CAA 798
 Thr Gln Glu Glu Leu Arg Gln Met Met Gln Pro Asp Asn Gly Leu Gln
 205 210 215
 TGG TCG CCG TGG TTT CGC ATC ATC GCC GCG CGC TTC CTT GAG CGC TGG 846
 Trp Ser Pro Trp Phe Arg Ile Ile Ala Ala Arg Phe Leu Glu Arg Trp
 220 225 230
 TGG GCT GAC CTA GAC GCG GCC CTG AAC ACT GAC AAA CAC GAG GAT TGG 894
 Trp Ala Asp Leu Asp Ala Ala Leu Asn Thr Asp Lys His Glu Asp Trp
 235 240 245 250
 GGA ACG GTG CAT CAC ATC AAC GAA GCG TGA AAACAG AAGCTGTAGG 940
 Gly Thr Val His His Ile Asn Glu Ala ***
 255
 ATGTCAAGAC ACGTCATGAG GGGGCTTGGC ATCTTGGCGG CTTCGTATCT CTTTTACTG 1000
 AGACTGAACC TGCAGCTGGA GACAATGGTG AGCCCAATTC AACTTCCGC TGCACTGGAA 1060
 AAAAAAAAAA AAAA 1074

SEQUENCE ID No.: 6

LENGTH: 1058

SEQUENCE TYPE: nucleic acid

STRANDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: genomic DNA

ORIGIN

ORGANISM: *Saccharomyces cerevisiae*

STRAIN: S288C

SEQUENCE CHARACTERISTIC

CHARACTERISTIC CODE: CDS

LOCATION: 187..1050

DETERMINATION METHOD: S

SEQUENCE:

TCGATGGGGG TTGCCTTTCT TTTTCGGTCT TAACTCCATT TATATTTATT TATTCATTTT 60

TATCTATTTA ACAGGAAACA GTTTTCTAGT GACAAGAAGG CGTATATCCC ACTTAATTCA 120

ATATTAGAGT ATTCGTATTT GGAATACAGG AAGAGTAAAA ATAAGCCAAA AATTCATTAC 180

ACCTCA ATG ACT GCC GAC AAC AAT AGT ATG CCC CAT GGT GCA GTA TCT AGT 231

Met Thr Ala Asp Asn Asn Ser Met Pro His Gly Ala Val Ser Ser

5 10 15

TAC GCC AAA TTA GTG CAA AAC CAA ACA CCT GAA GAC ATT TTG GAA GAG 279

Tyr Ala Lys Leu Val Gln Asn Gln Thr Pro Glu Asp Ile Leu Glu Glu

20 25 30

TTT CCT GAA ATT ATT CCA TTA CAA CAA AGA CCT AAT ACC CGA TCT AGT 327

Phe Pro Glu Ile Ile Pro Leu Gln Gln Arg Pro Asn Thr Arg Ser Ser

35 40 45

GAG ACG TCA AAT GAC GAA AGC GGA GAA ACA TGT TTT TCT GGT CAT GAT 375

Glu Thr Ser Asn Asp Glu Ser Gly Glu Thr Cys Phe Ser Gly His Asp

50 55 60

GAG GAG CAA ATT AAG TTA ATG AAT GAA AAT TGT ATT GTT TTG GAT TGG 423

Glu Glu Gln Ile Lys Leu Met Asn Glu Asn Cys Ile Val Leu Asp Trp

65 70 75

GAC GAT AAT GCT ATT GGT GCC GGT ACC AAG AAA GTT TGT CAT TTA ATG 471

Asp Asp Asn Ala Ile Gly Ala Gly Thr Lys Lys Val Cys His Leu Met

80 85 90 95

GAA AAT ATT GAA AAG GGT TTA CTA CAT CGT GCA TTC TCC GTC TTT ATT 519

Glu Asn Ile Glu Lys Gly Leu Leu His Arg Ala Phe Ser Val Phe Ile

100 105 110

TTC AAT GAA CAA GGT GAA TTA CTT TTA CAA CAA AGA GCC ACT GAA AAA 567

Phe Asn Glu Gln Gly Glu Leu Leu Leu Gln Gln Arg Ala Thr Glu Lys

115 120 125

5 ATA ACT TTC CCT GAT CTT TGG ACT AAC ACA TGC TGC TCT CAT CCA CTA 615
 Ile Thr Phe Pro Asp Leu Trp Thr Asn Thr Cys Cys Ser His Pro Leu
 130 135 140
 TGT ATT GAT GAC GAA TTA GGT TTG AAG GGT AAG CTA GAC GAT AAG ATT 663
 Cys Ile Asp Asp Glu Leu Gly Leu Lys Gly Lys Leu Asp Asp Lys Ile
 145 150 155
 10 AAG GGC GCT ATT ACT GCG GCG GTG AGA AAA CTA GAT CAT GAA TTA GGT 711
 Lys Gly Ala Ile Thr Ala Ala Val Arg Lys Leu Asp His Glu Leu Gly
 160 165 170 175
 ATT CCA GAA GAT GAA ACT AAG ACA AGG GGT AAG TTT CAC TTT TTA AAC 759
 15 Ile Pro Glu Asp Glu Thr Lys Thr Arg Gly Lys Phe His Phe Leu Asn
 180 185 190
 AGA ATC CAT TAC ATG GCA CCA AGC AAT GAA CCA TGG GGT GAA CAT GAA 807
 Arg Ile His Tyr Met Ala Pro Ser Asn Glu Pro Trp Gly Glu His Glu
 195 200 205
 ATT GAT TAC ATC CTA TTT TAT AAG ATC AAC GCT AAA GAA AAC TTG ACT 855
 Ile Asp Tyr Ile Leu Phe Tyr Lys Ile Asn Ala Lys Glu Asn Leu Thr
 210 215 220
 25 GTC AAC CCA AAC GTC AAT GAA GTT AGA GAC TTC AAA TGG GTT TCA CCA 903
 Val Asn Pro Asn Val Asn Glu Val Arg Asp Phe Lys Trp Val Ser Pro
 225 230 235
 30 AAT GAT TTG AAA ACT ATG TTT GCT GAC CCA AGT TAC AAG TTT ACG CCT 951
 Asn Asp Leu Lys Thr Met Phe Ala Asp Pro Ser Tyr Lys Phe Thr Pro
 240 245 250 255
 TGG TTT AAG ATT ATT TGC GAG AAT TAC TTA TTC AAC TGG TGG GAG CAA 999
 35 Trp Phe Lys Ile Ile Cys Glu Asn Tyr Leu Phe Asn Trp Trp Glu Gln
 260 265 270
 TA GAT GAC CTT TCT GAA GTG GAA AAT GAC AGG CAA ATT CAT AGA ATG 1047
 Leu Asp Asp Leu Ser Glu Val Glu Asn Asp Arg Gln Ile His Arg Met
 275 280 285
 CTA TAA CAACG 1058
 Leu ***

Claims

- 50 1. A DNA chain having characteristic of increasing carotenoid production, and containing the nucleotide sequence which encodes the polypeptide having the amino acid sequence substantially described in SEQUENCE ID No. 1, or a DNA chain which hybridizes with said DNA chain.
- 55 2. A DNA chain having characteristic of increasing carotenoid production, and containing the nucleotide sequence which encodes the polypeptide having the amino acid sequence substantially described in SEQUENCE ID No. 2, or a DNA chain which hybridizes with said DNA chain.
3. A method for producing carotenoid characterized by introducing DNA chain described in one of claim 1 or 2 into carotenoid-producing microorganisms, culturing said transformed microorganism and obtaining higher-carotenoid

content in the culture broth and cells .

4. A method for producing carotenoid characterized by introducing DNA chain containing the nucleotide sequence which encodes the polypeptide having the amino acid sequence substantially described in SEQUENCE ID No. 3, or DNA chain which hybridizes with said DNA chain introducing to carotenoid-producing microorganism, culturing said transformed microorganism and obtaining higher carotenoid content in the culture broth and cells .

FIG. 1

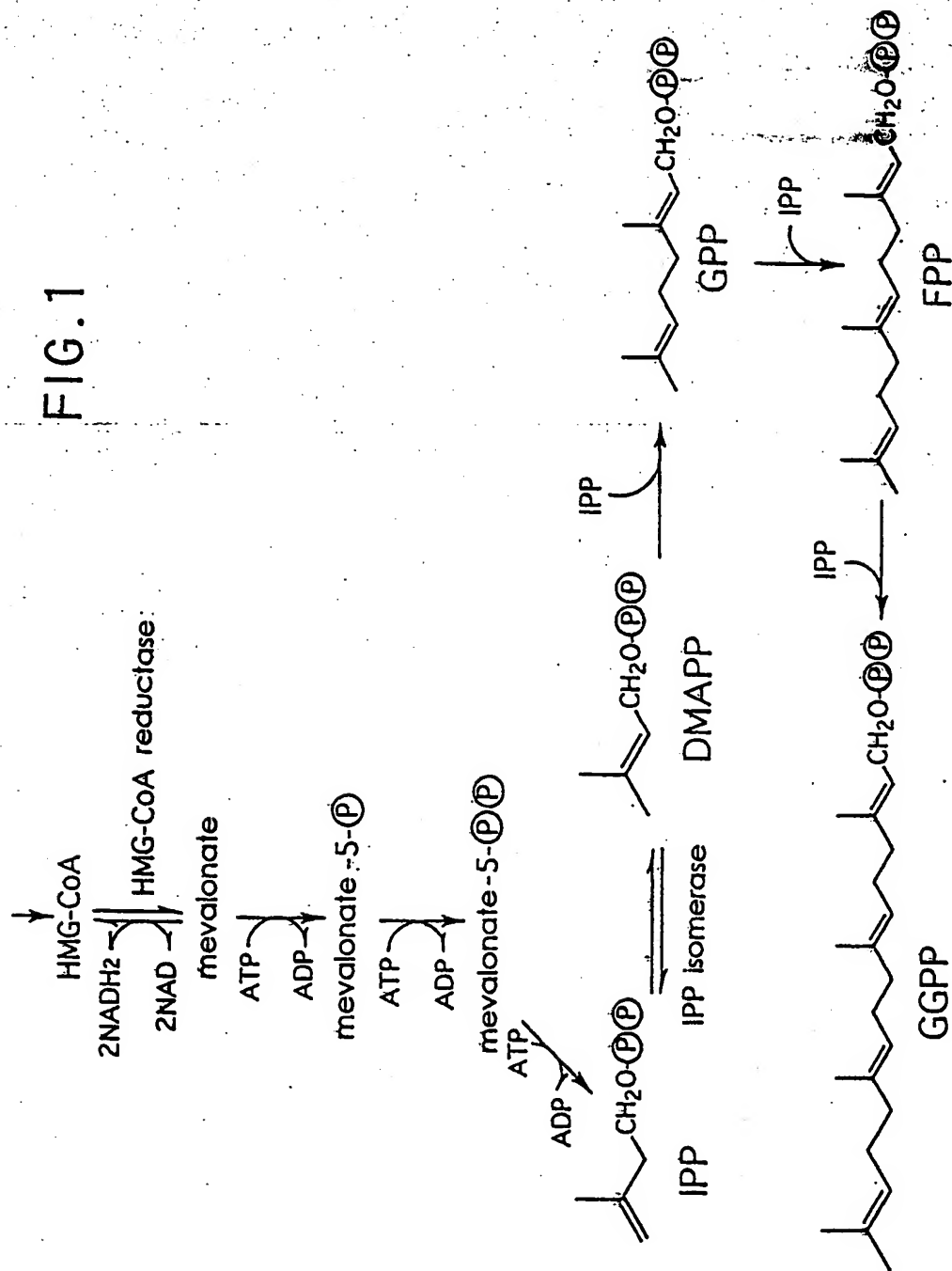


FIG. 2

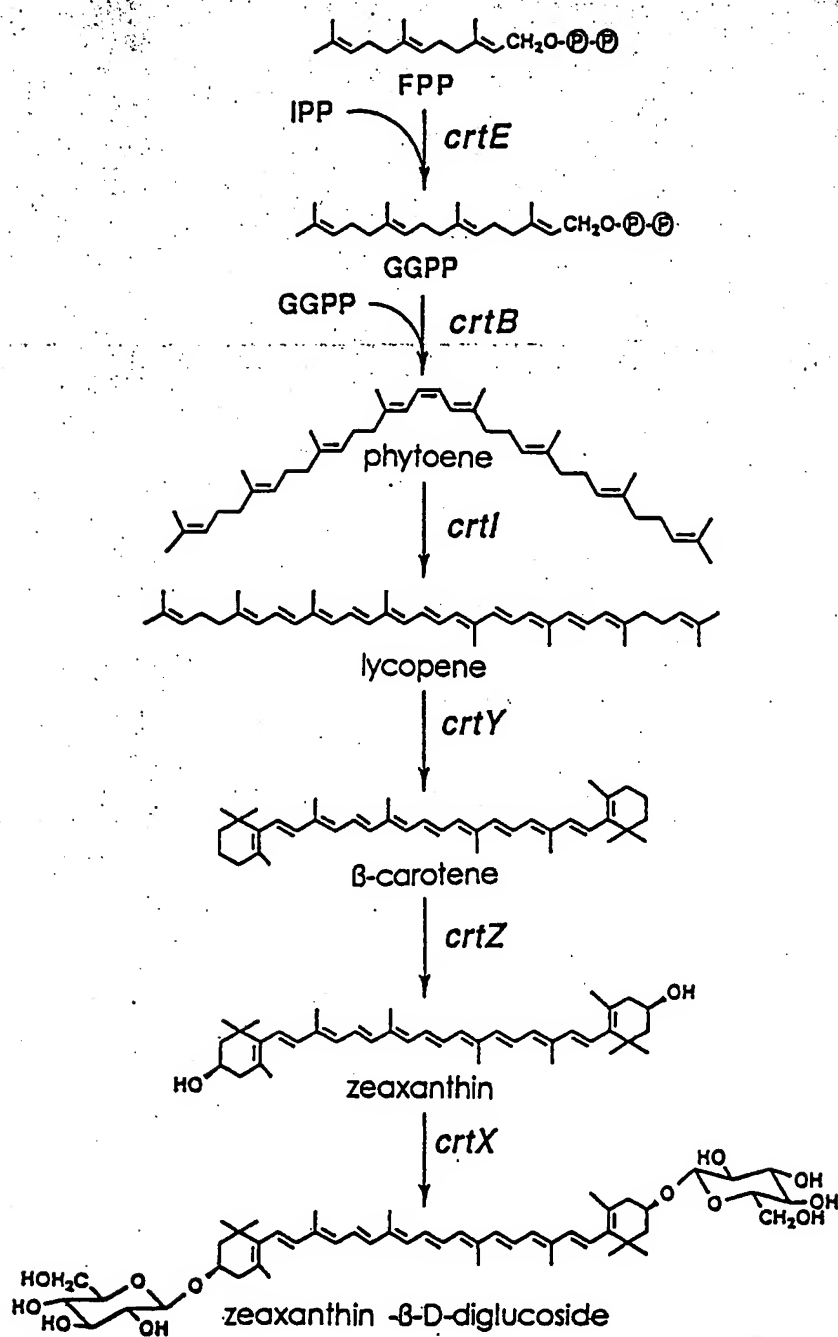


FIG. 3

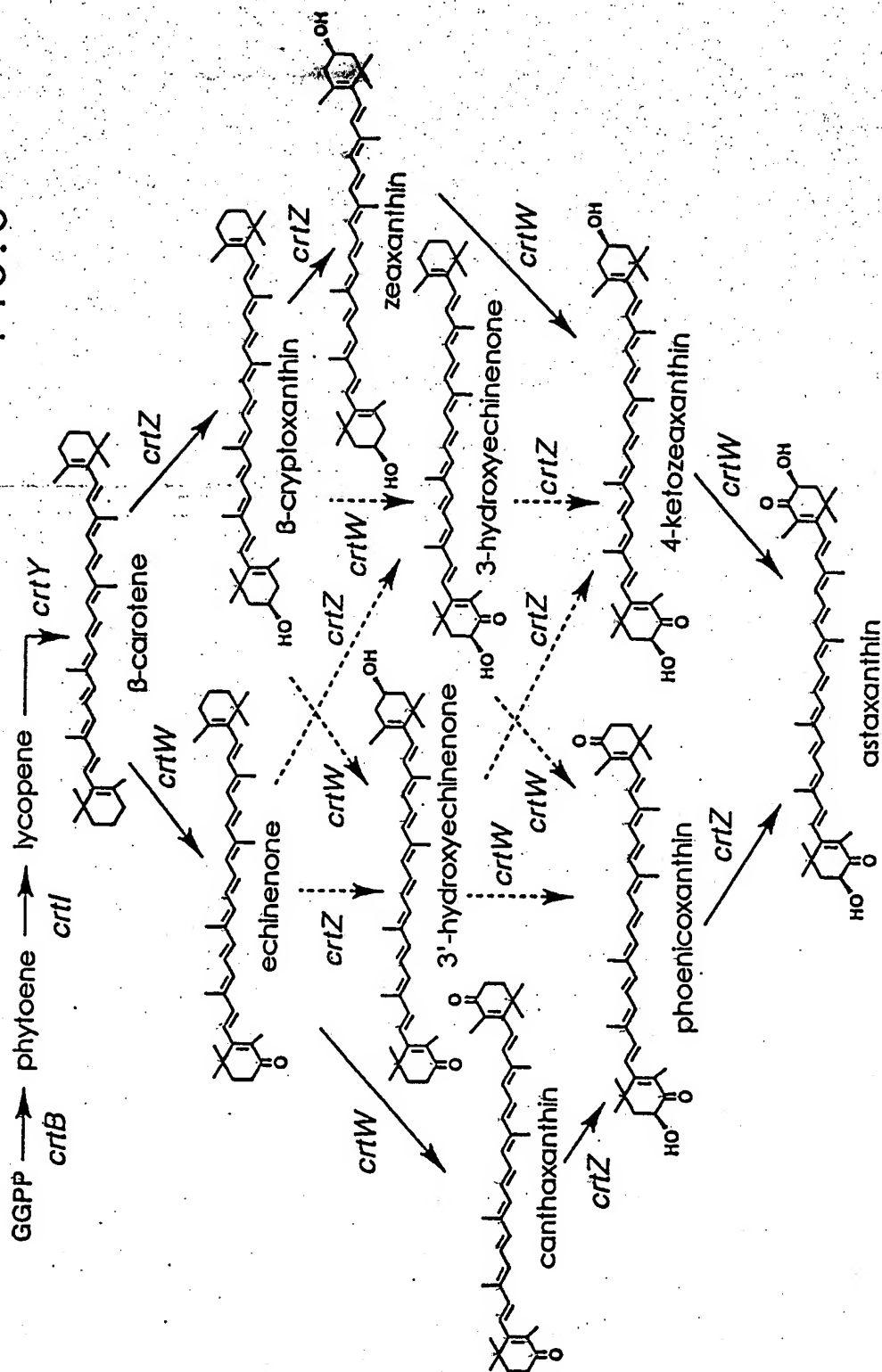


FIG. 4

A
 ↓
 9 18 27 36 45 54
 ATG TCC ATG CCC AAC ATT GTT CCC CCC GCC GAG GTC CGA ACC GAA GGA CTC AGT
 Met Ser Met Pro Asn Ile Val Pro Pro Ala Glu Val Arg Thr Glu Gly Leu Ser
 63 72 81 90 99 108
 TTA GAA GAG TAC GAT GAG GAG CAG GTC AGG CTG ATG GAG GAG CGA TGT ATT CTT
 Leu Glu Glu Tyr Asp Glu Glu Gln Val Arg Leu Met Glu Glu Arg Cys Ile Leu
 117 126 135 144 153 162
 GTT AAC CCG GAC GAT GTG GCC TAT GGA GAG GCT TCG AAA AAG ACC TGC CAC TTG
 Val Asn Pro Asp Asp Val Ala Tyr Gly Glu Ala Ser Lys Lys Thr Cys His Leu
 171 180 189 198 207 216
 ATG TCC AAC ATC AAC GCG CCC AAG GAC CTC CTC CAC CGA GCA TTC TCC GTG TTT
 Met Ser Asn Ile Asn Ala Pro Lys Asp Leu Leu His Arg Ala Phe Ser Val Phe
 225 234 243 252 261 270
 CTC TTC CCG CCA TCG GAC GGA GCA CTC CTG CTT CAG CGA AGA GCG GAC GAG AAG
 Leu Phe Arg Pro Ser Asp Gly Ala Leu Leu Leu Gln Arg Arg Ala Asp Glu Lys
 279 288 297 306 315 324
 ATT ACG TTC CCT GGA ATG TGG ACC AAC ACG TGT TGC AGT CAT CCT TTG AGC ATC
 Ile Thr Phe Pro Gly Met Trp Thr Asn Thr Cys Cys Ser His Pro Leu Ser Ile
 333 342 351 360 369 378
 AAG GGC GAG GTT GAA GAG GAG AAC CAG ATC GGT GTT CGA CGA GCT GCG TCC CGA
 Lys Gly Glu Val Glu Glu Glu Asn Gln Ile Gly Val Arg Arg Ala Ala Ser Arg
 387 396 405 414 423 432
 AAG TTG GAG CAC GAG CTT GGC GTG CCT ACA TCG TCG ACT CCG CCC GAC TCG TTC
 Lys Leu Glu His Glu Leu Gly Val Pro Thr Ser Ser Thr Pro Pro Asp Ser Phe
 441 450 459 468 477 486
 ACC TAC CTC ACT AGG ATA CAT TAC CTC GCT CCG AGT GAC GGA CTC TGG GGA GAA
 Thr Tyr Leu Thr Arg Ile His Tyr Leu Ala Pro Ser Asp Gly Leu Trp Gly Glu
 495 504 513 522 531 540
 CAC GAG ATC GAC TAC ATT CTC TTC TCA ACC ACA CCT ACA GAA CAC ACT GGA AAC
 His Glu Ile Asp Tyr Ile Leu Phe Ser Thr Thr Pro Thr Glu His Thr Gly Asn
 549 558 567 576 585 594
 CCT AAC GAA GTC TCT GAC ACT CGA TAT GTC ACC AAG CCC GAG CTC CAG GCG ATG
 Pro Asn Glu Val Ser Asp Thr Arg Tyr Val Thr Lys Pro Glu Leu Gln Ala Met
 198

FIG. 5

603	612	621	630	639	648
TTT GAG GAC GAG TCT AAC TCA TTT ACC CCT TGG TTC AAG TTG ATT GCC CGA GAC					
Phe Glu Asp Glu Ser Asn Ser Phe Thr Pro Trp Phe Lys Leu Ile Ala Arg Asp					
					216
657	666	675	684	693	702
TTC CTG TTT GGC TGG TGG GAT CAA CTT CTC GCC AGA CGA AAT GAA AAG GGT GAG					
Phe Leu Phe Gly Trp Trp Asp Gln Leu Leu Ala Arg Arg Asn Glu Lys Gly Glu					
					234
711	720	729	738	747	756
GTC GAT GCC AAA TCG TTG GAG GAT CTC TCG GAC AAC AAA GTC TGG AAG ATG TAG					
Val Asp Ala Lys Ser Leu Glu Asp Leu Ser Asp Asn Lys Val Trp Lys Met ***					
					251
					B

FIG.6

C
 ↓
 9 18 27 36 45 54
 ATG CAG CTG CTT GCC GAG GAC CGC ACA GAC CAT ATG AGG GGT GCA AGT ACC TGG
 Met Gln Leu Leu Ala Glu Asp Arg Thr Asp His Met Arg Gly Ala Ser Thr Trp
 18
 63 72 81 90 99 108
 GCA GGC GGG CAG TCG CAG GAT GAG CTG ATG CTG AAG GAC GAG TGC ATC TTG GTG
 Ala Gly Gly Gln Ser Gln Asp Glu Leu Met Leu Lys Asp Glu Cys Ile Leu Val
 36
 117 126 135 144 153 162
 GAT GCT GAC GAC AAC ATT ACA GGC CAT GTC AGC AAG CTG GAG TGC CAC AAG TTC
 Asp Ala Asp Asp Asn Ile Thr Gly His Val Ser Lys Leu Glu Cys His Lys Phe
 54
 171 180 189 198 207 216
 CTA CCA CAT CAG CCT GCA GGC CTG CTG CAC CGG GCC TTC TCT GTA TTC CTG TTT
 Leu Pro His Gln Pro Ala Gly Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe
 72
 225 234 243 252 261 270
 GAC GAC CAG GGG CGA CTG CTG CTG CAA CAG CGT GCA CGA TCA AAA ATC ACA TTC
 Asp Asp Gln Gly Arg Leu Leu Leu Gln Gln Arg Ala Arg Ser Lys Ile Thr Phe
 90
 279 288 297 306 315 324
 CCC AGT GTG TGG ACC AAC ACC TGC TGC AGC CAC CCT CTA CAT GGG CAG ACC CCA
 Pro Ser Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu His Gly Gln Thr Pro
 108
 333 342 351 360 369 378
 GAT GAG GTG GAC CAA CTA AGC CAG GTG GCC GAC GGC ACA GTA CCT GGC GCA AAG
 Asp Glu Val Asp Gln Leu Ser Gln Val Ala Asp Gly Thr Val Pro Gly Ala Lys
 126
 387 396 405 414 423 432
 GCT GCT GCC ATC CGC AAG TTG GAG CAC GAG CTG GGG ATA CCA GCG CAC CAG CTG
 Ala Ala Ala Ile Arg Lys Leu Glu His Glu Leu Gly Ile Pro Ala His Gln Leu
 144
 441 450 459 468 477 486
 CCG GCC AGC GCG TTT CGC TTC CTC ACG CGT TTG CAC TAC TGC GCC GCG GAC GTG
 Pro Ala Ser Ala Phe Arg Phe Leu Thr Arg Leu His Tyr Cys Ala Ala Asp Val
 162
 495 504 513 522 531 540
 CAG CCG GCT GCG ACA CAA TCA GCA CTC TGG GGC GAG CAC GAA ATG GAC TAC ATC
 Gln Pro Ala Ala Thr Gln Ser Ala Leu Trp Gly Glu His Glu Met Asp Tyr Ile
 180
 549 558 567 576 585 594
 TTA TTC ATC CGG GCC AAC GTC ACC CTT GCG CCC AAC CCT GAC GAG GTG GAC GAA
 Leu Phe Ile Arg Ala Asn Val Thr Leu Ala Pro Asn Pro Asp Glu Val Asp Glu
 198

FIG. 7

603	612	621	630	639	648
GTC AGG TAC GTG ACG CAG GAG GAG CTG CGG CAG ATG ATG CAG CCG GAC AAT GGG					
Val Arg Tyr Val Thr Gln Glu Glu Leu Arg Gln Met Met Gln Pro Asp Asn Gly					
					216
657	666	675	684	693	702
TTG CAA TGG TCG CCG TGG TTT CGC ATC ATC GCC GCG CGC TTC CTT GAG CGC TGG					
Leu Gln Trp Ser Pro Trp Phe Arg Ile Ile Ala Ala Arg Phe Leu Glu Arg Trp					
					234
711	720	729	738	747	756
TGG GCT GAC CTA GAC GCG GCC CTG AAC ACT GAC AAA CAC GAG GAT TGG GGA ACG					
Trp Ala Asp Leu Asp Ala Ala Leu Asn Thr Asp Lys His Glu Asp Trp Gly Thr					
					252
765	774	780			
GTG CAT CAC ATC AAC GAA GCG TGA					
Val His His Ile Asn Glu Ala***					
		259↑			
		D			

FIG.8

E
 ↓
 ATG ACT GCC GAC AAC AAT AGT ATG CCC CAT GGT GCA GTA TCT AGT TAC GCC AAA
 Met Thr Ala Asp Asn Asn Ser Met Pro His Gly Ala Val Ser Ser Tyr Ala Lys
 18
 63 72 81 90 99 108
 TTA GTG CAA AAC CAA ACA CCT GAA GAC ATT TTG GAA GAG TTT CCT GAA ATT ATT
 Leu Val Gln Asn Gln Thr Pro Glu Asp Ile Leu Glu Glu Phe Pro Glu Ile Ile
 36
 117 126 135 144 153 162
 CCA TTA CAA CAA AGA CCT AAT ACC CGA TCT AGT GAG ACG TCA AAT GAC GAA AGC
 Pro Leu Gln Gln Arg Pro Asn Thr Arg Ser Ser Glu Thr Ser Asn Asp Glu Ser
 54
 171 180 189 198 207 216
 GGA GAA ACA TGT TTT TCT GGT CAT GAT GAG GAG CAA ATT AAG TTA ATG AAT GAA
 Gly Glu Thr Cys Phe Ser Gly His Asp Glu Glu Gln Ile Lys Leu Met Asn Glu
 72
 225 234 243 252 261 270
 AAT TGT ATT GTT TTG GAT TGG GAC GAT AAT GCT ATT GGT GCC GGT ACC AAG AAA
 Asn Cys Ile Val Leu Asp Trp Asp Asp Asn Ala Ile Gly Ala Gly Thr Lys Lys
 90
 279 288 297 306 315 324
 GTT TGT CAT TTA ATG GAA AAT ATT GAA AAG GGT TTA CTA CAT CGT GCA TTC TCC
 Val Cys His Leu Met Glu Asn Ile Glu Lys Gly Leu Leu His Arg Ala Phe Ser
 108
 333 342 351 360 369 378
 GTC TTT ATT TTC AAT GAA CAA GGT GAA TTA CTT TTA CAA CAA AGA GCC ACT GAA
 Val Phe Ile Phe Asn Glu Gln Gly Glu Leu Leu Leu Gln Gln Arg Ala Thr Glu
 126
 387 396 405 414 423 432
 AAA ATA ACT TTC CCT GAT CTT TGG ACT AAC ACA TGC TGC TCT CAT CCA CTA TGT
 Lys Ile Thr Phe Pro Asp Leu Trp Thr Asn Thr Cys Cys Ser His Pro Leu Cys
 144
 441 450 459 468 477 486
 ATT GAT GAC GAA TTA GGT TTG AAG GGT AAG CTA GAC GAT AAG ATT AAG GGC GCT
 Ile Asp Asp Glu Leu Gly Leu Lys Gly Lys Leu Asp Asp Lys Ile Lys Gly Ala
 162
 495 504 513 522 531 540
 ATT ACT GCG GCG GTG AGA AAA CTA GAT CAT GAA TTA GGT ATT CCA GAA GAT GAA
 Ile Thr Ala Ala Val Arg Lys Leu Asp His Glu Leu Gly Ile Pro Glu Asp Glu
 180

FIG.9

549	558	567	576	585	594
ACT AAG ACA AGG GGT AAG TTT CAC TTT TTA AAC AGA ATC CAT TAC ATG GCA CCA					
Thr Lys Thr Arg Gly Lys Phe His Phe Leu Asn Arg Ile His Tyr Met Ala Pro					
					198
603	612	621	630	639	648
AGC AAT GAA CCA TGG GGT GAA CAT GAA ATT GAT TAC ATC CTA TTT TAT AAG ATC					
Ser Asn Glu Pro Trp Gly Glu His Glu Ile Asp Tyr Ile Leu Phe Tyr Lys Ile					
					216
657	666	675	684	693	702
AAC GCT AAA GAA AAC TTG ACT GTC AAC CCA AAC GTC AAT GAA GTT AGA GAC TTC					
Asn Ala Lys Glu Asn Leu Thr Val Asn Pro Asn Val Asn Glu Val Arg Asp Phe					
					234
711	720	729	738	747	756
AAA TGG GTT TCA CCA AAT GAT TTG AAA ACT ATG TTT GCT GAC CCA AGT TAC AAG					
Lys Trp Val Ser Pro Asn Asp Leu Lys Thr Met Phe Ala Asp Pro Ser Tyr Lys					
					252
765	774	783	792	801	810
TTT ACG CCT TGG TTT AAG ATT ATT TGC GAG AAT TAC TTA TTC AAC TGG TGG GAG					
Phe Thr Pro Trp Phe Lys Ile Ile Cys Glu Asn Tyr Leu Phe Asn Trp Trp Glu					
					270
819	828	837	846	855	864
CAA TTA GAT GAC CTT TCT GAA GTG GAA AAT GAC AGG CAA ATT CAT AGA ATG CTA					
Gln Leu Asp Asp Leu Ser Glu Val Glu Asn Asp Arg Gln Ile His Arg Met Leu					
					288
867					
TAA					F

FIG. 10

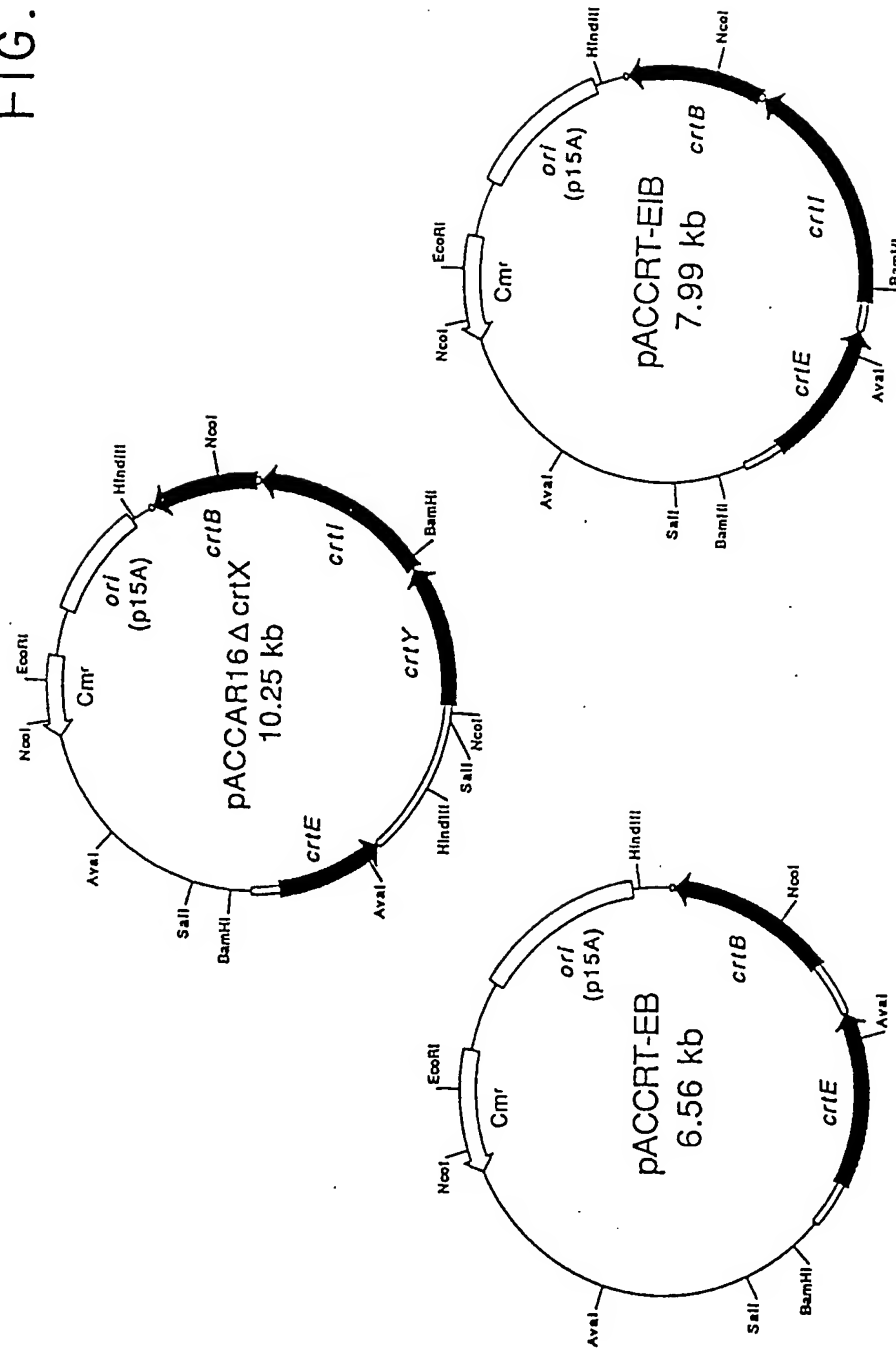
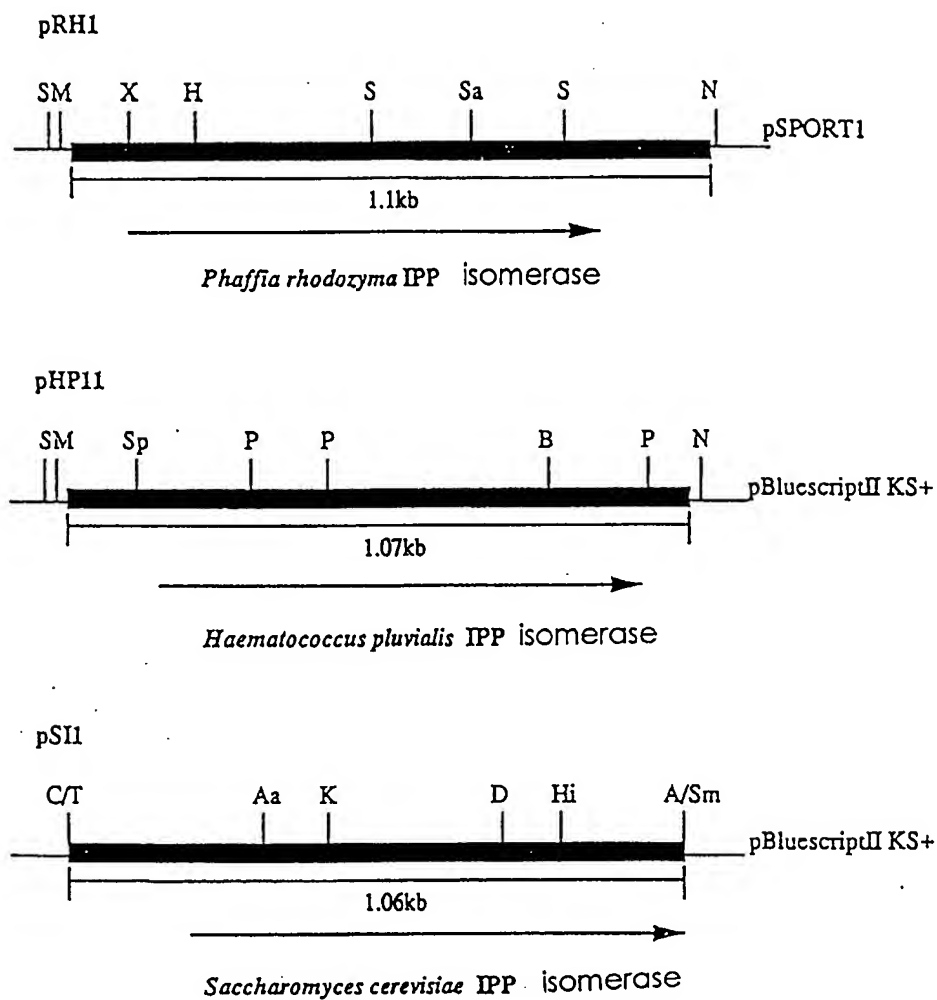


FIG. 11



Aa: AatII, A: AccII, B: BssHII, D: DraI, Hi: HincII,
 H: HpaI, K: KpnI, M: MluI, N: NotI, P: PstI, Sa: SacI,
 S: SalI, Sp: SphI, X: XbaI

FIG.12

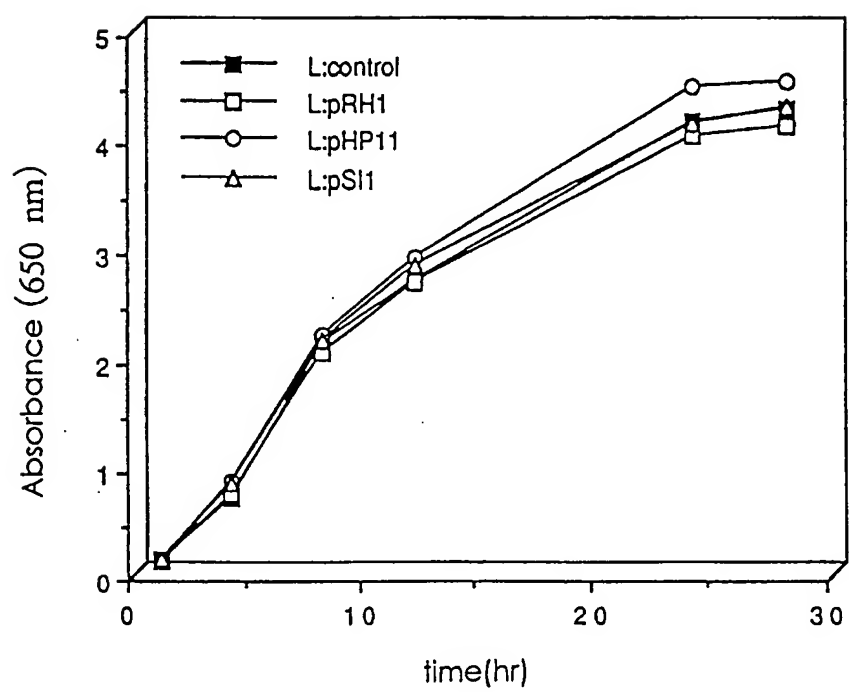


FIG. 13

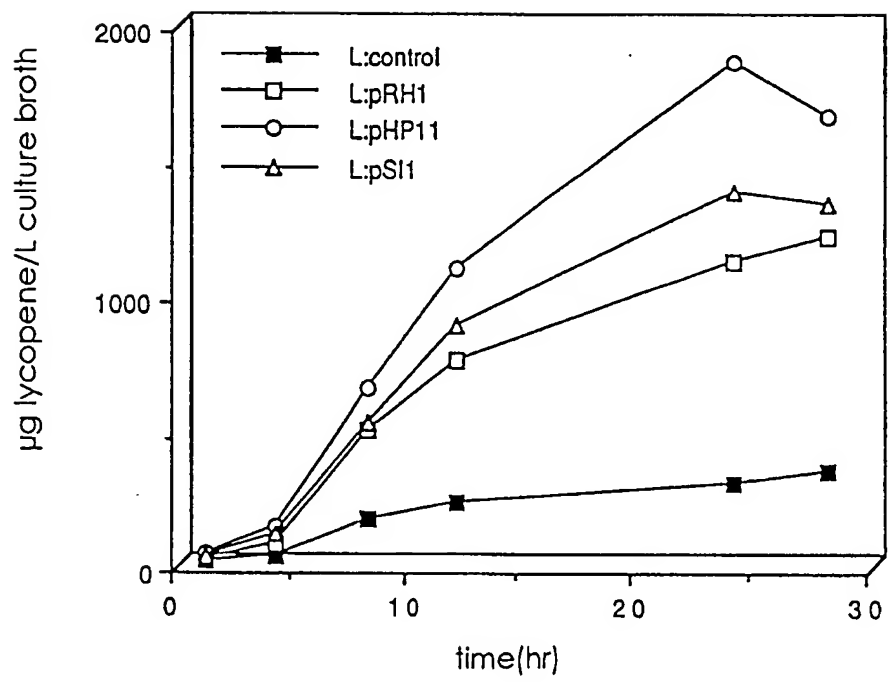


FIG. 14

E.coli	µg carotene/g dry weight	production ratio
L: control	228	1
L: pRH1	825	3.6
L: pHP11	1029	4.5
L: pSI1	859	3.8
β: control	488	1
β: pRH1	709	1.5
P: control	246	1
P: pRH1	413	1.7
P: pHP11	504	2.1

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP96/00574

A. CLASSIFICATION OF SUBJECT MATTER Int. C1 ⁶ C12N15/00, C12N9/90 According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) Int. C1 ⁶ C12N15/00, C12N9/90 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) BIOSIS PREVIEWS, CAS		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Chu-Biao Xue "A Covalently Constrained Congener of the Saccharomyces cerevisiae Tridecapeptide Mating Pheromone Is an Aronist" J. Biol. Chem., Vol. 264, No. 32, p. 19161-19168	1 - 4
A	Ian P. street "Isopentenylidiphosphate: Dimethylallyldiphosphate Isomerase: Construction of a High-Level Heterologous Expression System for the Gene from Saccharomyces cerevisiae and Identification of an Active-site Nucleophile" Biochemistry, Vol. 29, p. 7351-7538	1 - 4
<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "A" document member of the same patent family		
Date of the actual completion of the international search June 3, 1996 (03. 06. 96)		Date of mailing of the international search report June 11, 1996 (11. 06. 96)
Name and mailing address of the ISA/ Japanese Patent Office Facsimile No.		Authorized officer Telephone No.

Form PCT/ISA/210 (second sheet) (July 1992)